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Title:
Perfect score:
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Sequence 60, Appli Sequence 6, Appli Sequence 72, Appl Sequence 95, Appl Sequence 35, Appl Sequence 35, Appl	58087 2710, 448, 88810 13067 14, Ap	2719, A 411, Ap 2717, A 380, Ap 71125, 29077,	1132, 348, A 348, A 355, A 165, A 163, A 163, A 165, A 165, A 165, A 1349, 2720, 2720, 376, A	e 2678, e 2938, e 108, e 7449, e 735, p e 734, p e 849, e 849, p e 849,	Description Sequence 2, Appli Sequence 538, App Sequence 538, App Sequence 538, App

ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/09/292,437
CURRENT FILING DATE: 1999-04-15
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 621
TYPE: DNA
ORGANISM: Staphylococcus aureus
US-09-292-437-2
RESULT 2
US-08-781-986A-538/c
; Sequence 538, Application US/08781986A
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GENERAL INFORMATION:
APPLICANT: Olaf Schneewind
APPLICANT: Sarkis Mazmanian
APPLICANT: Gwen Liu
APPLICANT: Hung Ton-That
TITLE OF INVENTION: IDENTIFICATION OF SO
FILE REFERENCE: 510015.213
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                                                                                                                                                                                                                                                                                                                                                                  actttcattgaccgtccgaactatcaatttacaaatcttaaagcagccaaaaaaggtagt
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                                                                                                                                                                        ttaattacttgtgatgattacaatgaaaagacaggcgtttgggaaaaacgtaaaatcttt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gctgatattaaagaaccagtatatccaggaccagcaacacctgaacaattaaatagaggt
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Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (301) 309-851
TELEFAX: (301) 309-8512
INFORMATION FOR SEO ID NO: 'S
SEQUENCE CHARACTERISTICS:
LENGTH: 3733 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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MEDIUM TYPE: Diskette, 3
COMPUTER: HP Vectura 486/
OPERATING SYSTEM: MSDOS
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: PB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION: NAME: Benson, Bob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
421 atggtgtactttaaagttggtaatgaaacacgtaagtataaaatgacaagtataagagat
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ZIP: 208
                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                               aagattgaacaatatgataaaaatgtaaaaagaacaggcgagtaaagataaaaagcagcaa 180
                                                               actttcattgaccgtccgaactatcaatttacaaatcttaaagcagccaaaaaaggtagt
                                                                                                                                                                                gctgatattaaagaaccagtatatccaggaccagcaacacctgaacaattaaatagaggt
                                                                                                                                                                                                                                      gctaaacctcaaattccgaaagataaatcgaaagtggcaggctatattgaaattccagat
                                              ACTTTCATTGACCGTCCGAACTATCAATTTACAAATCTTAAAGCAGCCAAAAAAAGGTAGT
                                                                                                       GTAAGCTTTGCAGAAGAAAATGAATCACTAGATGATCAAAATATTTCAATTGCAGGACAC
                                                                                                                                                                 GCTGATATTAAAGAACCAGTATATCCAGGACCAGCAACACCTGAACAATTAAATAGAGGT
                                                                                                                                                                                                                           GCTAAACCTCAAATTCCGAAAGATAAATCGAAAGTGGCAGGCTATATTGAAATTCCAGAT
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6/33
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Pred. No. 1.2e-106;
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US-08-956-171-538/c
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GENERAL INFORMATION:
GENERAL INFORMATION:
Charles Kunsch
TITLE OF INVENTION: Staphylococcu
NUMBER OF SEQUENCES: 5255
                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                    TELEFAX: (301) 309-851 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                 REEERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
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OPERATING SYSTEM:
SOFTWARE: ASCII T
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REGISTRATION NUMBER:
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                             aagattgaacaatatgataaaaatgtaaaagaacaggcgagtaaagataaaaagcagcaa 180
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               AAGATTGAACAATATGATAAAAATGTAAAAGAACAGGCGAGTAAAGATAAAAAGCAGCAA
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                                                                                                                                                                                                     100.0%; Score 621; DB 13; 100.0%; Pred. No. 1.2e-106;
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5255
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                                                                              APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                 SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and NUMBER OF SEQUENCES: 5255
                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Charles Kunsch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gtagctacagaagtcaaataa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ttaattacttgtgatgattacaatgaaaagacaggcgtttgggaaaaacgtaaaatcttt 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gttaagcctacagatgtaggagttctagatgaacaaaaaggtaaagataaacaattaaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          actttcattgaccgtccgaactatcaatttacaaatcttaaagcagccaaaaaaggtagt 420
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                                    NAME: HOOVER, Kenley K. REGISTRATION NUMBER: 40, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                        FILING DATE: 20-Oct-1997 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                          ZIP:
                                                                                                                                                                                                                                                                                                                                                  STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                   APPLICATION NUMBER: US/08/956,1718
                                                                                                                                                                                                                                                OPERATING
                                                                                                                                                                                                                                                                COMPUTER:
                                                                                                                                                                                                                                                                                                                                     STATE: Maryland
             TELEPHONE:
TELEFAX: (301)
                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Human
                                                                                                                                                                                                                                                                                                           20850
                                                                                                                                                                                                                                                                                                                                                                                                                                          Steven C. Barash
Michael R. Fannon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patrick S. Dillon
Craig A. Rosen
                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                 SYSTEM: MSDOS version
                                                                                                                                                                                                                                                                HP Vectra 486/33
             (301)
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US-08-827-356-2678; Sequence 2678, Application US/08827356; GENERAL INFORMATION:
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US-08-956-171B-538
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Best Local
                                                                         APPLICANT: George H. Shimer, Jr.
APPLICANT: George H. Miller
APPLICANT: Roberta S. Hare
APPLICANT: ROBERTA S. HARE
TITLE OF INVENTION: STAPHYLOCOCCUS AU
TITLE OF INVENTION: COMPOSITIONS AND
NUMBER OF SEQUENCES: 5574
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                                                     CORRESPONDENCE ADDRESS:
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                                ADDRESSEE:
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Nes 621; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RMATION FOR SEQ ID NO: 538:
SEQUENCE CHARACTERISTICS:
LENGTH: 3733 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gttaagcctacagatgtaggagttctagatgaacaaaaaggtaaagataaacaattaaca
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STRANDEDNESS: double
       2000
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  Schering-Plough Corporation
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                                                                                                                              AUREUS RELATED
                                                                                                     METHODS
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Best Local Similarity
Matches 615; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATA:
PRIOR APPLICATION NUMBER: 60/014,477
APPLICATION NUMBER: 60/016,743
FILING DATE: 02-MAY-1996
FILING DATE: 02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60
FILING DATE: 14-JUN-11
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Staphylococcus FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
     481
                                                     424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/0 FILING DATE: 01-APR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 07033-0530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      atggtgtactttaaagttggtaatgaaacacgtaagtataaaatgacaagtataagagat 480
                                                                                                                                                actttcattgaccgtccgaactatcaatttacaaatcttaaagcagccaaaaaaggtagt 420
                                                                                                                                                                                                                                                                      gtaagctttgcagaagaaaatgaatcactagatgatcaaaaatatttcaattgcaggacac 360
                                                                                                                                                                                                                                                                                                                                                                      gctgatattaaagaaccagtatatccaggaccagcaacacctgaacaattaaatagaggt 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aagattgaacaatatgataaaaatgtaaaagaacaggcgagtaaagataaaaagcagcaa 180
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                                                                                                                                                                                                                                                                                                                                             GCTGATATTAAAGAACCAGTATATCCAGGACCAGCAACACCTGAACAATTAAATAGAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTAAACCTCAAATTCCGAAAGATAAATCAAAAGTGGCAGGCTATATTGAAATTCCAGAT 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGATTGAACAATATGATAAAAATGTAAAAGAACAGGCGAGTAAAGACAATAAGCAGCAA
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PC-DOS/MS-DOS
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Pred. No. 6.1e-105;
0; Mismatches 6;
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CURRENT APPLICATION NUMBER: US/09/611,529
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/417,811
PRIOR APPLICATION NUMBER: US 09/233,718
PRIOR APPLICATION NUMBER: US 09/253,718
PRIOR APPLICATION NUMBER: US 09/266,557
PRIOR APPLICATION NUMBER: US 09/266,557
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 09/266,556
PRIOR APPLICATION NUMBER: US 09/266,556
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 09/266,542
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US-09-611-529-2938
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APPLICANT: George H. Miller
APPLICANT: Roberta S. Hare
APPLICANT: Karen J. Shaw
TITLE OF INVENTION: Staphylococcus aureus
TITLE OF INVENTION: 1034/1C963US1
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J4, 108

LATION NUMBER: US 09/266,557

RILING DATE: 1999-03-11

RICH APPLICATION NUMBER: US 09/266,555

RICH EILING DATE: 1999-03-11

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FILING DATE: 1990

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FILING DATE: 1900
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OR APPLICATION NUMBER: US 09/266,541
OR FILING DATE: 1999-03-11
OR APPLICATION NUMBER: US 09/037,934
OR FILING DATE: 1998-03-10
OR APPLICATION NUMBER: US 09/036,720
OR FILING DATE: 1998-03-06
OR APPLICATION NUMBER: US 09/036,338
OR APPLICATION NUMBER: US 09/036,338
                                                                      FILING DATE: 1990-04 OR APPLICATION NUMBER: US 6
APPLICATION NUMBER: US 6
TITME DATE: 1996-05-02
                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 09/035,079
FILLING DATE: 1998-03-06
APPLICATION NUMBER: US 09/035,079
APPLICATION NUMBER: US 09/035,013
                            APPLICATION NUMBER: US EFILING DATE: 1996-06-14
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R OF SEQ ID
NO 2938
TH: 624
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1998-03-06
NUMBER:
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IUMBER: US 08/831,156
1997-04-01
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1998-03-06
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UMBER: US 09/036,081
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Best Local Similarity 99.0%;
Matches 615; Conservative
                                                                                           APPLICANT: George H. Shimer, Jr.
APPLICANT: George H. Miller
APPLICANT: Roberta S. Hare
APPLICANT: Roberta S. Hare
APPLICANT: Raren J. Shaw
TITLE OF INVENTION: NUCLEOTIDE SEQUENCE OF A
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS
TITLE OF INVENTION: GENOME AND RELATED
TITLE OF INVENTION: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 112
                                                                           CORRESPONDENCE ADDRESS
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                            STREET:
CITY: K
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            New Jersey
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                                           Schering-Plough Corporation 000 Galloping Hill Road
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Pred. No. 6.1e
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EQ ID NO LENGTH:

COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS

PatentIn

MEDIUM TYPE:

READABLE FORM: TYPE: Floppy disk

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Best Local Similarity
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LOCATION: 1...91077
-08-831-156A-108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15161 ATGAAAAATGGACAAATCGATTAATGACAATCGCTGGTGTAGTACTTATCCTAGTGGCA 15220
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INFORMATION FOR SEQ ID NO: 1
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PRIOR APPLICATION DATA:
00/014,477
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                           481
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FILING DATE: 01-APR-1996
APPLICATION NUMBER: 60/016,743
FILING DATE: 02-MAY-1996
APPLICATION NUMBER: 60/020,016
FILING DATE: 14-JUN-1996
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TYPE: nucleic acid
STRANDEDNESS: double
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             gttaagcctacagatgtaggagttctagatgaacaaaaaggtaaagataaaccaattaaca
                                                                                                                                                                                                                                                                                             gcatatttgtttgctaaaccacatatcgataattatcttcacgataaagataaagatgaa 120
                                                     GTAAGCTTTGCAGAAGAAATGAATCACTAGATGATCAAAATATTTCAATTGCAGGACAC
                                                                                                                                                                                                                                                                                                                                                                     aagattgaacaatatgataaaaatgtaaaagaacaggcgagtaaagataaaaagcagcaa
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GTTAAGCCAACAGATGTAGAAGTTCTAGATGAACAAAAAGGTAAAGATAAACAATTAACA
                                                                                                                ACTTTCATTGACCGTCCGAACTATCAATTTACAAATCTTAAAGCAGCCAAAAAAAGGTAGT
                                                                                                                               actttcattgaccgtccgaactatcaatttacaaatcttaaagcagccaaaaaaaggtagt
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01-APR-1997
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Pred. No. 1.2e-104;
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; ORGANISM: Staphylococcus aureus US-09-611-529-7449
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                                                          NUMBER OF SEQ ID SEQ ID NO 7449
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                                                                      PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1996-06-14 NUMBER OF SEQ ID NOS: 7451
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CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/417,811
PRIOR FILING DATE: 1999-10-14
PRIOR APPLICATION NUMBER: US 09/353,718
PRIOR APPLICATION NUMBER: US 09/266,557
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                           LENGTH: 81
TYPE: DNA
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R FILLING DATE: 1999-03
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APPLICATION NUMBER: US
FILING DATE: 1999-03-11
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PTITING DATE: 1996-04-01
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FILING DATE: 1997-04-01
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George H. Miller
Roberta S. Hare
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N: Staphylococcus aureus Related Compositions and Methods
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UMBER: US 09/266,541
1999-03-11
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JMBER: US 60/014,477
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JMBER: US_09/036,079
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UMBER: US 09/036,720
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1998-03-06
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                                                                                                                                                     Sequence 735, Application US/60038697
GENERAL INFORMATION:
APPLICANT: Lagace, Robert E.
APPLICANT: Corley, Neil C.
APPLICANT: Russo, Frank D.
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF STAPHLOCOCCUS AUREUS
TITLE OF INVENTION: GENOME, FRAGMENTS THEREOF, AND USES THEREOF
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for 1
                                                                                                                        NUMBER OF SEQUENCES: 1027
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS,
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                                                                                   STREET: 3174 POI
CITY: PALO ALTO
STATE: CALIFORN
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                                                              ZIP: 94304
                                                                        COUNTRY:
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Pred. No. 1.5e-104;
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US-60-038-697-735
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REGISTRATION NUMBER: 93,132
REFERENCE/DOCKET NUMBER: P0-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 855-055
TELEPHONE: (415) 845-4166
INFORMATION FOR SEQ ID NO: 735:
SEQUENCE CHARACTERISTICS:
LENGTH: 45487 base pairs
TYPE: nucleic acid
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Best Local Similarity
Matches 574; Conserv
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IMMEDIATE SOURCE:
CLONE: SAC0735
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FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C
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ttaattacttgtgatgattacaatgaaaagacaggcg 577
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                                                         GTTAAGCCTACAGATGTAGAAGTTCTGGATGAACAAAAAGGTAAAGATAAACAATTAACA
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Pred. No. 2.3e-97;
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45450 540 45390 240

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RESULT 10
US-60-046-714-734
Sequence 734, Application US/60046714
GENERAL INFORMATION:

APPLICANT:

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Best Local :
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IMMEDIATE SOURCE:
CLONE: SAU1c734
                                                                                                                                                                                                                                               45032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 845-4166
INFORMATION FOR SEQ ID NO: 734:
SEQUENCE CHARACTERISTICS:
                                                                                                                          45152
                                                                                                                                                                                    45092
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APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/60/046,714
FILING DATE: HEREWITH
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PM-0001-1P
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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CORRESPONDENCE ADDRESS:
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Russo, Frank D.
Heath, Joe D.
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SEQ ID NO 849
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Best Local Similarity
Matches 547; Conserva
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APPLICANT: Thornton, Michael
TITLE OF INVENTION: POLYNUCLEOTIDES OF
FILE REFERENCE: PA-0016 US
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CURRENT FILING DATE: 2000-07-20
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OTHER INFORMATION: 813650849
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Application US/09620608
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MBER: 60/144,883
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CURRENT FILING DATE: 1999-07-20
NUMBER OF SEQ ID NOS: 1973
SOFTWARE: PERL Program
SEQ ID NO 849
LENGTH: 551
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APPLICANT: Nuttal, Rachel
APPLICANT: Thornton, Michael
TITLE OF INVENTION: POLYNUCLEOTIDES OF STAPHYLOCOCCUS
FILE REFERENCE: PA-0016 P
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OTHER INFORMATION: 8136
PUBLICATION INFORMATION:
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ORGANISM: Staphylococcus
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Pred. No. 1.7e-90;
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US-09-450-969-1132, Application US/09450969
; Sequence 1132, Application US/09450969
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
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US-09-450-969-1:132
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CURRENT FILING DATE: 1999-11-29
NUMBER OF SEO ID NOS: 7544
SEO ID NO 1132
LENGTH: 612
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73.1%;
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Pred. No. 3.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; DB 18;
3.4e-54;
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US-60-068-228-360
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                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (650) 845-4166
NFORMATION FOR SEQ ID NO: 360:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDJUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
                                                                                                                                                                            2109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,1
                                       2220
                                                                                                         2160 TCGACGCCAAAGATACCTTCCGATAAATCTAAAATGGCTGGTTATATAGAAGTTCCAGAC
                                                                                                                                                                                                                                               2049 ATTTATTTATTCTCAAAAGCCATATATCGATAATTATCTACATGAAAAAGATAACGATCAT 2108
                                                                                                                                                                                                                                                                                                                  1989 ATGAAGCAGTGGATGAATAGATTAATCACCTTAATAGGCGTATTGTTAATCATTTTAGCT 2048
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CLONE: SEP1c361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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                                                                                                                           181 gctaaacctcaaattccgaaagataaatcgaaagtggcaggctatattgaaattccagat 240
                                                                                                                                                                                            121 aagattgaacaatatgataaaaatgtaaaagaacaggcgagtaaagataaaaagcagcaa 180
301 gtaagctttgcagaagaaaatgaatcactagatgatcaaaatatttcaattgcaggacac 360
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CITY: PALO ALTO
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VENTION: NUCLEOTIDE SEQUENCES OF STAPHYLOCOCCUS
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ER: PM-0002-4 P
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Pred. No. 2.2e-52;
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US-60-038-081-348
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                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lagace, Robert E.
APPLICANT: Corley, Neil C.
APPLICANT: Russo, Frank D.
TITLE OF INVENTION: HUCLEOTIDE SEQUENCES OF STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS GENOME, FRAGMENTS THEREOF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 31, STREET: PALO ALTO CITY: PALO ALTO CALIFORNIA
                                                  STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                IMMEDIATE SOURCE:
CLONE: SE1c0348
                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
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                                                                                                                                                                                                                                                      REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                          NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94304
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                                                                                                                       LENGTH:
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                                                                                                    nucleic acid
                                                                                                                                                                                                                                                                    CERRONE, MICHAEL C
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                                                                                                                                                                               (415) 845-4166
                                                                   linear
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                                                    CDNA
                                                                                     single
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Query Match
Best Local Similarity

53.4%; 73.2%;

Score 331.4; | Pred. No. 2.2e 0; Mismatches

DB 28; 2e-52;

Indels

10;

Gaps

2

Length 11434;

Matches

Conservative

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600 tgtagctacagaagtcaaataa 621
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2586 CATAGCTACACAAATTAACTAA 2607
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                                         GCACAAATAAAAGAACCAGTATACCCTGGTCCAGCAACACCAGAACAACTCAATAGAGGT 2285
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                                                                                                                                                                            ACGTTTACAGATCGTTCGCACTATCAATTTACAAATTTAAAATCAGCCAAAATCGGTAGT 2405
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Search completed: March 14, 2001, 15:06:48 Job time: 4688 sec

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Perfect score:
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ALIGNMENTS

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V74849 standard; DNA; 3733 BP

V74849;

Staphylococcus

aureus contig SEQ ID #538

16-MAR-1999

(first entry)

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misc_feature Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; 30-JUL-1997 Staphylococcus EP786519-A2 misc_feature toxic shock syndrome; aureus /*tag= b
/note= "these bases represent a line of missing text in
 the sequence listing in the specification. They
 are included to maintain the nucleotide numbering
 given in the specification for this DNA sequence" Location/Qualifiers 721..780 ds.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents one of 5191 Staphylococcus aureus DNA sequences CC of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using CC that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are CC likely to encode antigens have been identified and these polypeptides can CC be used in a vaccine composition against S.aureus infection. The CC saureus in a sample. S.aureus is implicated in numerous human diseases, CC including cellulitis, eyelid infections, food poisoning, osteomyelitis, concluding cellulitis, eyelid infections, scalded skin syndrome, toxic shock CC syndrome, etc. Organisms transformed with the DNA sequences can be used CC for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating CC computer readable medium.
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                                                                            T05868 encodes a chicken leucocytozoan immunogenic protein, or a fragment of it can be used in a recombinant vaccine to against chicken leucocytozoan disease. The DNA is used in a and operatively linked to an expression regulatory sequence
                                                                                                                                                  Chicken leucocytozoan immunogenic protein - vaccine against chicken leucocytozoan disease
                                                 Sequence 3399 BP; 1577 A;
                                                                                                                              Claim 6; Page 6-9; 35pp; Japanese
                                                                                                                                                                                          WPI; 1996-006311/01.
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(KITA ) KITASATO KENKYUSHO SH.
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Q87587-89 encode polypeptides having a whole or partial epitope of structural protein of Leucocytozoan protozoa (see R70491-93). The polypeptides and DNA encoding them are useful in the production of
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                                                                                                                                 WPI; 1995-167252/22, P-PSDB; R70491.
                                                                                                                                                                                                                                                                                                                                                                               DNA encoding Leucocytozoan protozoa
                                                                                                                                                                                                                                                                                                                                                                                                                                     Q87587
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q87587 standard;
                                                      Claim 1;
                                                                                                                                                                                                             10-SEP-1993;
                                                                                                                                                                                                                                                               04-APR-1995
                                                                                                                                                                                                                                                                                          JP07089995-A
                                                                                                                                                                                                                                                                                                                 Leucocytozoan
                                                                                                                                                                                                                                                                                                                                           leucocytozoan protozoa; struc-
leucocytozoanosis; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                            19-DEC-1995
                                                                                                                                                                      (DOBU-) DOBUTSUYO SEIBUTSUGAKUTEKI SEIZAI KYOKAI.
(NISS-) NISSEIKEN KK.
                                                                                                                                                                                                                                     10-SEP-1993;
                                                                                       mmune inducing polypeptide against Leucocytozoan protozoa - n production of vaccines for treatment of leucocytozoanosis
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                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                 protozoa
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        WO8601802-A
                                    exon
                                                                                 Plasmodium
                                                                                                                     Sequence encoding the ring-infected Erythrocyte Surface Antigen (RESA).
                                                                                                                                                24-AUG-1991
                                                                                                 Malaria vaccine; antigen; epitope;
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11-SEP-1984;
10-SEP-1985;
            X33181;
                                                                                   4186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleotide sequence corresp. to all or a portion of the base sequence coding RESA (N60472) or FRA (N60473). RESA and FIRA antigenicity suitable for providing protective immunity against plasmodium falciparum malarial infections.
                             X33181 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA coding for Plasmodi
poly:peptide(s) having
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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85AU-0047326.
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l.6e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0 other;
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3914 250 3854

3795

131

191

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71

ttgctaaaccacatatcgataattatcttcacgataaagataaagatgaaaagattgaac 130

Query Match
Best Local Similarity
Matches 244; Conserv

Conservative

0;

Score 59.8; DB 20 Pred. No. 0.00038; 0; Mismatches 307

307; 20;

Indels Length 6644;

0;

Gaps

0;

9.6%;

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cell line into which an apoptosis resistance gene has been introduced.
The recombinant viruses generated are capable of expressing apoptosis-
associated genes. These can then be used in a variety of diseases for
which the induction of apoptosis by gene transfer, or where the
inhibition of harmful apoptosis, is therapeutic. The recombinant viruses
are useful as vectors for gene therapy which can be applied to cancer
therapy for destroying cancer cells selectively, the treatment of
autoimmune diseases and graft rejection reaction, and apoptosis induction
therapy for inflammatory cells in inflammatory diseases. Prior arts have
encountered the problem where if an adenovirus vector capable of
expressing an apoptosis-associated gene is introduced into animal cells,
the cells producing the virus will be destroyed because the period of
time required to induce cell death apoptosis is shorter than that
required to replicate and produce the virus, resulting in failure to
obtain a recombinant virus having the integrated apoptosis-associated
gene. In this invention an apoptosis-resistant 293 cell line (having an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cowpox virus; bsr; viral vector; expression; apoptosis; resistance; crmA; bcl-2; bcl-x1; FLIP; survivin; IAP; ILP; adenovirus; cancer; autoimmune disease; graft rejection reaction; inflammation; inflammatory disease; ss.
Sequence
                                    apoptosis resistant gene introduced) is established and overcomes the problem. The present sequence represents the base sequence of the plasmid pRx-ires-bsr, which contains the cowpox virus bsr gene, and is used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New apoptosis-resistant virus-sensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (RPRG-) RPR GENCELL ASIA PACIFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1999-243728/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Page 38-41; 51pp; English.
6644 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                              invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the plasmid pRx-ires-bsr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97JP-0259235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98WO-JP04010
2166 A; 1573 C; 1424 G;
                                                                                                                                                                                                                                                                                                                                                                                                                              describes an apoptosis-resistant virus-sensitive
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1481
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0 other;
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cell line into which an apoptosis resistance gene has been introduced. The recombinant viruses generated are capable of expressing apoptosis-associated genes. These can then be used in a variety of diseases for which the induction of apoptosis by gene transfer, or where the inhibition of harmful apoptosis, is therapeutic. The recombinant viruses are useful as vectors for gene therapy which can be applied to cancer therapy for destroying cancer cells selectively, the treatment of autoimmune diseases and graft rejection reaction, and apoptosis induction therapy for inflammatory cells in inflammatory diseases. Prior arts have
                                                                                                                                                                                                                                                                                                                                                                                                                                           Cowpox virus; bsr; viral vector; expression; apoptosis; resistance; crmA; bcl-2; bcl-xl; FLIP; survivin; IAP; ILP; adenovirus; cancer; autoimmune disease; graft rejection reaction; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3915
                                                                                                                      The present invention describes an apoptosis-resistant virus-sensitive
                                                                                                                                                                                                                                                                                                           07-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cowpox virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4275
                                                                                                                                                 Example 2; Page 41-45;
                                                                                                                                                                                                                                                                                                                                     18-MAR-1999
                                                                                                                                                                                                                                                                                                                                                               WO9913073-A2
                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                inflammatory disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Base sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X33182 standard;
                                                                                                                                                                                                                                                         (RPRG-) RPR GENCELL ASIA PACIFIC
                                                                                                                                                                                                                                                                                                                                                                                         HOMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               491
                                                                                                                                                                           apoptosis-resistant virus-sensitive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         accgtccgaactatcaatttacaaatcttaaagcagccaaaaaaaggtagtagtatggtgtact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cagaagaaaatgaatcactagatgatcaaaatatttcaattgcaggacacactttcattg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bsr; viral vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the plasmid pRx-Bcl-xl-bsr
                                                                                                                                                                                                                                                                                    97JP-0259235.
                                                                                                                                                                                                                                                                                                            98WO-JP04010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      621
                                                                                                                                              51pp;
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                                                                                                                                                 English
                                                                                                                                                                          cell
                 induction
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WWW XEXTX AX

25-JUN-1999

(first

entry)

X33180

standard;

DNA;

ВP

Cowpox virus bsr full length gene sequence

Cowpox virus; bsr; viral vector; expression; apoptosis; resistance; crmA; bcl-2; bcl-xl; FLIP; survivin; IAP; ILP; adenovirus; cancer; autoimmune disease; graft rejection reaction; inflammation;

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RESULT
X33180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encountered the problem where if an adenovirus vector capable of expressing an apoptosis-associated gene is introduced into animal cells, the cells producing the virus will be destroyed because the period of time required to induce cell death by apoptosis is shorter than that required to replicate and produce the virus, resulting in failure to obtain a recombinant virus having the integrated apoptosis-associated gene. In this invention an apoptosis-resistant 293 cell line (having an apoptosis resistant gene introduced) is established and overcomes the
                                                                                                              4943
                                                                                                                                                                      4883
                                                                                                                                                                                                                             4823
                                                                                                                                                                                                                                                                                                                                                                                                  4643
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                                                         5003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7372 BP; 2353 A; 1749 C; 1649 G; 1621 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        problem. The present sequence represents the base sequence of the plasmid pRx-Bcl-xl-bsr, which contains the human Bcl-xl gene, and is used in an example from the present invention.
                                                                                  611
                                                                                                                                                                                                 491
                                                                                                                                                                                                                                                                                                                                                                                                                              251
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              7
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                                                                                                                                                                                                                                         ttaaagitggtaatgaaacacgtaagtataaaatgacaagtataagagatgttaagccta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aatatgataaaaatgtaaaagaacaggcgagtaaagataaaaagcagcaagctaaacctc
                                                         aaaaaaaaaa
                                                                                                              gtgatgattacaatgaaaagacaggcgtttgggaaaaacgtaaaatctttgtagctacag
                                                                                                                                                                   accgtccgaactatcaatttacaaatcttaaagcagccaaaaaaggtagtatggtgtact
                                                                                                                                                                                                                                                                                                                                        cagaagaaaatgaatcactagatgatcaaaatatttcaattgcaggacacactttcattg
                                                                                                                                                                                                                                                                                                                                                                                                ttyctaaaccacatatcgataattatcttcacgataaagataaagatgaaaagattgaac 130
                                                                                                                                                                                                                           Conservative
                                                                                  621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s 59.8; DB 20;
. No. 0.00039;
ismatches 307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                                                                                                                                                                              430
                                                                                                                                                                                                                                                                                                                                                                                                4702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           190
                                                                                                                                                                                                                           4882
                                                                                                                                                                                                                                                                                  4822
                                                                                                                                                                                                                                                                                                                                          4762
                                                                                                                                                                                                                                                                                                                                                                                                                                                       4642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC The recombinant viruses generated are capable of expressing apoptosis.

CC associated genes. These can then be used in a variety of diseases for which the induction of apoptosis, is therapeutic. The recombinant viruses can then be used in a variety of diseases for combination of harmful apoptosis, is therapeutic. The recombinant viruses care useful as vectors for gene therapy which can be applied to cancer therapy for distances and graft rejection reaction, and apoptosis induction concurred the problem where if an adenovirus vector capable of cancer can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
  5188
                                                                                                                                                                                                                                                                                                                                                                4948
                                                                                                                                                                                                                                                                                                                                                                                                                                                         4888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7797 BP; 2542 A; 1760 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes an apoptosis resistant virus sensitive cell line into which an apoptosis resistance gene has been introduced.
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                                                                                                                                                                                                                                                                                                                                                                                                             131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 34-38; 51pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New apoptosis-resistant virus-sensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (RPRG-) RPR GENCELL ASIA PACIFIC INC
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                                                                                                                                                                                                                                                                                                                      191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     used in an example from the present invention.
                                                                                                             cagaagaaaatgaatcactagatgatcaaaatatttcaattgcaggacacactttcattg 370
                                                                                                                                                                                                                                                                                               aaattccgaaagataaatcgaaagtggcaggctatattgaaattccagatgctgatatta
                                                                                                                                                                                                                                                                                                                                                                                     ttgctaaaccacatatcgataattatcttcacgataaagataaagatgaaaagattgaac 130
accgtccgaactatcaatttacaaatcttaaaagcagccaaaaaaaggtagtatggtgtact 430
                                                                                                                                                                                                      aagaaccagtatatccaggaccagcaacactgaaccaattaaatagaggtgtaagctttg
                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97JP-0259235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98WO-JP04010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 59.8; DB 20; Pred. No. 0.00039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1656 G; 1839 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 7797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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CC The recombinant viruses generate are capture of capture of the capture of capture of capture of associated genes. These can then be used in a variety of diseases for cc which the induction of apoptosis by gene transfer, or where the cc inhibition of harmful apoptosis, is therapeutic. The recombinant viruses care useful as vectors for gene therapy which can be applied to cancer cc therapy for destroying cancer cells selectively, the treatment of cautoimmune diseases and graft rejection reaction, and apoptosis induction ct therapy for inflammatory cells in inflammatory diseases. Prior arts have encountered the problem where if an ademovirus vector capable of cc expressing an apoptosis associated gene is introduced into animal cells, the cells producing the virus will be destroyed because the period of time required to induce cell death by apoptosis is shorter than that combinant virus having the virus, resulting in failure to obtain a recombinant virus having the integrated apoptosis-associated gene. In this invention an apoptosis-resistant 293 cell line (having an apoptosis resistant gene introduced) is established and overcomes the
   RESULT
X33184
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                                                                                                                                                                                                                                                                                        The present invention describes an apoptosis-resistant virus-sensitive cell line into which an apoptosis resistance gene has been introduced. The recombinant viruses generated are capable of expressing apoptosis-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cowpox virus; bsr; viral vector; expression; apoptosis; resistance; crmA; bcl-2; bcl-xl; FLIP; survivin; IAP; ILP; adenovirus; cancer; autoimmune disease; graft rejection reaction; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5248
                                                                                                                                                                                                                                                                                                                                                                  Example 3; Page 46-49; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-243728/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-SEP-1998;
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                                               WO9022811-A
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                                                                                                                                    Location/Qualifiers
1..2352
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                                                                                          /product=GLURP
                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA;
                                                                                                                                                                                                                                                                                                 carboxylic terminal part of native GLURP
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                                                                                                                                                                                                                                                    vaccine; GLURP;ss
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Matches 239;

Conservative

Mismatches

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Query Match
                                                                                                                             content of codons for glutamate. Three major repetitive sequences are: one motif from bp 34 to bp 156 is repeated from bp 289 to bp 411; another motif from bp 477 to bp 521 is repeated tandemly twice from bp 1232 to bp 566 and from bp 567 to bp 611; a third motif from bp 1174 to bp 1233 is repeated tandemly 11 times. This last repetitious region consists of 360bp repeats differing only in 3 bases GAT coding for aspartate. This region is flanked to the 5' terminal od a degenerated 60 bp repeat. GC content of the coding part of the insert is on average 30%, and of the non-coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dziegiel
Jakobsen
                                                                                                                                                                                                                                                                   insert to a "TĀA" stop codon. It is longest ORF found in the sequence. Sequence displays some of the characteristics of other malaria nucleic acid sequences: tandemly repeated motifs, high AT content and a corresponding preference for codons containing these bases, and a high
                                                                                                                                                                                                                                                                                                                                                                                                      Polypeptide(s) derived from Plasmidium falciparum antigen -vaccines and in production of antibodies, for diagnosis and therapy of malaria.
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03-MAR-1989;
                                                                                  Sequence 3095 BP; 1443 A; 300 C; 491 G;
                                                                                                                                                                                                                                                                                                                                        An open reading frame of 2349 bps extends from the 5'
                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 7; 108pp; English
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                   Local Similarity
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89DK-0005191
                 9.18;
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Score 56.6; DB 11;
Pred. No. 0.0016;
0; Mismatches 304;
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                      agatgtaggagttctagatgaacaaaaaggtaaagataaacaattaacattaatttg
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tgaagaaattctaccagaagataaaaatgaaaaagttcaacatgaaatagtagaggttga 1739
                                                                                    tgaagaaattctaccagaagataaaaatgaaaaaggtcaacatgaaatagtagaggt 1679
                                                                                                               taaagttggtaatgaaacacgtaagtataaaatgacaagtataagagatgttaagcctac
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                                                                                                                                                                                                         ccgtccgaactatcaatttacaaatcttaaagcagccaaaaaaggtagtattgtgtactt
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                                                             Matches
                                                                             Query Match
Best Local :
                                                                                                                                                                              This sequence corresponds to the coding sequence for a Plasmodium falciparum strain KI pre-erythrocytic liver stage antigen-3 (LSA-3) protein. The gene sequence was isolated by screening a P. falciparum strain T9/96 library with serum from a missionary treated by prophylaxis (for strain T6/96 see FR9101286). Of 20 clones isolated, clone 7295 was used to screen a library generated from Thai strain KI. One clone contained a 6.85 kb insert including the genomic sequence T78867. The gene comprises a 1.8 kb region encoding 3 major blocks of 4 amino acid repeats and a 3' hydrophobic region corresponding to a 91ycosyl-phosphatidylinositol membrane anchoring sequence. The invention relates to new polypeptides of at least 10 amino acids derived from the LSA-3 polypeptide with the exception of the peptides W24791-4. The LSA-3 peptides can be used to raise antibodies and as vaccines for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmodium falciparum; pre-erythrocyte; liver stage antigen; serum; prophylaxis; Thai strain; gene organisation; exon; intron; hydrophob; glycosyl-phosphatidylinositol membrane anchoring sequence; antibody; vaccine; immunotherapy; malaria; ds.
Plasmodium falciparum poly:peptide(s) and related nucleic acids derived from the liver stage antigen-3, useful for malaria vacci prodn. and diagnosis
                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                  Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-JUN-1995;
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                  | 104 | ataaagataaagatgaaaagattgaacaatatgataaaaatgtaaaaagaacaggcgagta 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         612 agt
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                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                               20; Fig
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                                                              Conservative
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                                                                                                                                        BP;
                                                                                                                                                                      of malaria.
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                                                                                                                                       2388 A; 431 C;
                                                                           9.1%;
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                                                           Score 56.6; D
Pred. No. 0.00
0; Mismatches
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                                                              Indels
                                                                                        Length 5361;
                                                                                                                                       other;
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hydrophobic;
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                                                                                                                                                                                                                                                                                               prophylaxis; Thai strain; gene organisation; exon;
glycosyl-phosphatidylinositol membrane anchoring s
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          13-JUN-1995;
                                 12-JUN-1996;
                                                      27-DEC-1996.
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                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                    immunotherapy;
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          95FR-0007007
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                                                                                                                        /*tag= c
/number= 1
443..5602
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275..442
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77..274
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                                                                                                                                                                                                                                                                                                                                                                                                                 DNA;
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                                                                                                                                                                                                                                                                                                         pre-erythrocyte; liver stage antigen;
in: gene organisation; exon; intron; hy
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                                                                                                                                                                                                                                                                                                 anchoring sequence;
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;; antibody;
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Best Local :
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   5193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein (W24790). The gene sequence was isolated by screening a P. falciparum strain T9/96 library with the serum from a missionary treated by prophylaxis (for strain T6/96 see FR9101286). Of 20 clones isolated, clone 729S was used to screen a library generated from Thai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
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                  gggaaaaacgtaaaaatctttgtagctacaga
                                                                                 gtaaagataaacaattaacattaacttgtgatgattacaatgaaaaagacaggcgttt
                                                                                                                           acgtagacgaagtaatgaaatatgttcaaaaaattgataaagaagttgataaagaagtat
                                                                                                                                               aaatgacaagtataagagatgttaagcctacagatgtaggagttctagatgaacaaaaag
                                                                                                                                                                                                              acaa--
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                                                             ctaaagctttagaatcaaaaatgatgttactaatgttttaaaaacaaaatcaagattttt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 56.6; DE Pred. No. 0.001 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56.6; DB 1
                                 611
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T41852

ID T41852 standard; DNA; 97

AC T41852;

XX 20-FEB-1997 (first ent)

XX Plasmodium falciparum; (

KW detection; identifications

XX Plasmodium falciparum M

XX Plasmodium falcipa

ET misc_feature 5546.55

ET misc_feature 6254.65

ET misc_feature 62540.5

ET misc_feature 7449.6

PA (AFFY-) AFFYMAX TECHNO

PA (AFFY-) AFFYMAX TECHNO

PA (AFFY-) Baruch DI, Howard RJ,

XX PAPSDB; W00384.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA encoding Plasmodium falciparum erythrocyte membrane
  New Plasmodium falciparum erythrocyte membrane proteins -
                                                                                                    (AFFY-) AFFYMAX TECHNOLOGIES NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium falciparum MC type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               falciparum; erythrocyte membrane protein;
identification; treatment; prevention; pa
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                                                                                                                               95US-0430908
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                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_except= 6269..6271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transl_except= 6263..6265
                                                                                                                                                                                                                                                                                                     /transl_except= 6278..6280
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6257..6259
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6254..6256
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656..658
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2909..2911
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1754..8478
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        develop
malaria
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 epidemic relapsing fever; endemic relapsing fever; infection; diagnosis; characterisation; detection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7912
                             Borrelia burgdorferi; spirochete; bacterium;
                                                          Borrelia
                                                                                       04-MAY-1999
                                                                                                                                            X20248
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parasite
                                                        burgdorferi polynucleotide sequence
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                                                                                     (first entry)
                                                                                                                                            DNA;
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                             pathogen; Lyme disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated Borrelia burgdorferi nucleic acids - used to products for the detection, diagnosis, characterisation, and therapy of infections, particularly Lyme disease
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22-JUL-1997;
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                gtactttaaagttggtaatgaaacacgtaagtataaagtagacaagtataagagatgttaa
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97US-0053344.
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                                                                                                                                                           This sequence encodes the Plasmodium falciparum gp190/MSP-1 (merozoite surface protein). This gene is used in a method for stabilising the gene sequences by reducing the AT content. Such products are useful in vaccines against malaria or for producing monoclonal antibodies (for passive immunisation). The complete gp190 protein can now be produced outside the parasite and has, at least over extended regions, the native pattern of folding. Larger amounts of the protein can be produced recombinantly than would be possible using the parasites as source.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gp190;
   1418
                                                                                                                                                                                                                                                                                                   Recombinant production of complete gp190/MSP-1 Plasmodium surface protein - useful in anti-malaria vaccines, also stabilising genes
                                                                                                                                                                                                                                                                                                                                                                                                                  02-OCT-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum
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                                                                                                                                            Sequence 4940
                                                                                                                                                                                                                                                                      Example 1;
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           aagataaaagcagcaagctaaacctcaaattccgaaagataaatcgaaagtggcaggct
                                           cccttctaatgaaggaataataaacaatctaaaagaaaatcttaatgaaaaacgaaaaata
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onal antibody; passive immunisation; parasite; ss.
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45.9%;
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be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scaided skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polyment and surgical would infect the polyment and surgical would be sequenced with the DNA sequences can be used for recombinant production of the polyment and surgical would be sequenced with the DNA sequences.
                                                                                                                                              for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the S.aureus DNA sequences contained on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides of the process of the control of the
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Copyright (c) 1993 - 2000 Comp
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US-08-961-083-162
US-08-741-134-6
US-08-715-131-2
US-08-725-837-2
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US-08-630-349-6
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US-08-676-974-1
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Sequence 9, Appli	Sequence 9, Appli	Sequence 6, Appli	Sequence 2, Appli	Sequence 12, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 3, Appli	ა '	ω,	Sequence 3, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 6, Appli	Sequence 4, Appli	Sequence 6, Appli	Sequence 4, Appli

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US-08-961-083-162

Sequence 162,

Application US/08961083

Patent No. 6159469

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ADDRESSEE: HATTER
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APPLICANT: Choi et. al.

TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
                                                                                                                  TELEFAX: (301) 309-85: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: HP Vectra 41
OPERATING SYSTEM: MSDG
SOFTWARE: ASCII Text
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NAME: Brookes, A. Anders
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                                                                   amino acid
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                                                                                 223 amino acids
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                                 linear
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               protein
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309-8512
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64 QIPKDKSKVAGYIEIPDADIKEPVYPGPATPEQLNRGVSFAEENE-SLDDQNIS--IAGH 120

QVSDDPDAVYGYLSIPSLEIMEPVYLG-ADYHHLGMGLAHVDGTPLPLDGTGIRSVIAGH 110

52

Query Match
Best Local Similarity
Matches 45; Conserv

Conservative

23;

Mismatches

12.7%; 30.8%;

Score 137; Pred. No. 8

DB 3; .8e-07;

Length 223; Indels

Gaps

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                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 215-568-3439
                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/007,163
FILING DATE: 01-NOV-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 215-568-3100
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 335 LKNGKVFDKNTSGKPFAFKLGRGEVIKGWDIGVAGMSVGGERRIII 380
                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 411 amino acids
TYPE: amino acid
                                                                                                                                                  226 DNDGEEEQEEEEEEQKEEVKPEPKKSKKEKKRKHEEKEEEKKAK--KVKKVEFKKDLEE 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 LITCD---DYN-----EKTGVWEK 196
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                                                                         284 GPTKPKSKKEQDKHKPKSKVLEG-GIVIEDRTIGDGPQ-----AKRGARVGMRYIGK 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 R-AEPSHVFFRHLDQLKVGDALYYDNGQEIVEYQMMDTEIILPSEWEKLESVSSKN-IMT 168
                                                                                                           90 GPATPEQLNRGVSFAEENESLDDQNISIAGHTFIDRPNYQFTNLKAAKKGSMVYFK-VG- 147
                                                                                                                                                                                    30 DNYLHDKDKDEKIEQYDKNVKEQASKDKKQQAKPQIPKDKSKVAGYIEIPDADIKEPVYP 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: Windows 3.11 SOFTWARE: WordPerfect for Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER:
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VENTION: IMMUNOPHILIN FKBP46 AND COMPOSITIONS FOR MAKING
                                                                                                                                                                                                                                                                                                                                                                                                                                                        215-568-3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Litwack,
                                                                                                                                                                                                                             Conservative
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                                      -NETRK---YKMTSIRDVKPTDVGVLDEQKGKDKQLTL 181
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                                                                                                                                                                                                                                            8.3%;
21.1%;
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Emad S.
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37; Mis
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                                                                                                                                                                                                                                                           DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 8.2%;
Best Local Similarity 28.0%;
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INFORMATION FOR SEQ ID NO:
                    APPLICANT:
                                    APPLICANT:
                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                     129 IFAK-NIAKQLSAKDPNNK-EFYEKNLKEYTDKLDKLDKESKDKFNKIPAEKKLIVTSEG 186
                                                                                                                                                                                      242 MKTVSQDTNIPIYAQIFTD-----SIAEQGKEGDSYY
                                                                                                                                                                                                                                                        187
                                                                                                                                                                                                                                                                                         70
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TOPOLOGY: lin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: MS
SOFTWARE: ASCII Text
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                    Application US/08715131
                                                                                                                                                                                                                      ----NISIAGHTFIDRPNYQFTNLKAAKKGSMVYFKVGNETRKYKMTSIRD 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/08961083
Sampson, Jacquelyn S.
Russell, Harold
Tharpe, Jean A.
Ades, Edwin W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         289 amino acids
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APPLICANT: APPLICANT:

Carlone,

George M.

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Вb
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MOLECULE TYPE:
US-08-715-131-2
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                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08922837 Patent No. 5888770
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Best Local
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                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 14114.0200 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                  COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                           APPLICANT: Bryant, Alexander P. TITLE OF INVENTION: NO. 5888770el SpOIIIE NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                             APPLICANT: Chalker,,
APPLICANT: Feliu,, Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               114 -----NISIAGHTFIDRPNYQFTNLKAAKKGSMVYFKVGNETRKYKMTSIRD 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    207 AFKYFSKAYG---VPSAYIWEINTEEEGTPEQIKTLVEKLRQTKVPSLFVE--SSVDDRP 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149
                                                                                                                                                                                                                                                                                                                                                                                                              262 MKTVSQDTNIPIYAQIFTD-----SIAEQGKEGDSYY-----SMMKYNLDKIAE 305
                                                                                        STATE:
                                                                                                 STREET: 4000 BELL.
CITY: Philadelphia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Spratt, Gwendolyn D. REGISTRATION NUMBER: 36,016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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                                                     COUNTRY: USA
ZIP: 19103-2793
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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                                                                                        PA
                                                                                                                       E: Dechert, Price & Rhoads
                                                                                                                                                                                                                               Feliu,, Maria M.Z.
Brown,, James R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           309 amino acids
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127 Peachtree Street, Suite 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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IBM Compatible
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28.0%; Pred. No. 0.18;
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                                                                                                                                                                                                                                                                     Alison F.
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                                                                                                                                                                                                                                                     Sequence 2, Application US/09196857A Patent No. 6100069
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
APPLICANT: Warren, Richard L.
APPLICANT: Schilling, Lisa K.
TITLE OF INVENTION: No. 6100069el tig
                                                                                    APPLICANT: Debouck, Christine APPLICANT: Jaworski, Deborah D.
                                                                                                                    APPLICANT: Mooney, Jeffrey APPLICANT: Zhong, YiYi
                                                                                                                                                   APPLICANT: Throup, John P.
APPLICANT: Lawlor, Elizabeth J.
                                                                                                                                                                                      APPLICANT: Biswas, Sanjoy
                                                                                                                                                                                                         APPLICANT: Brown, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                      APPLICANT: Wang, Min
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FASTEM: DOS
SOFTWARE: FASTEEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          214 RRKEERFVKQEEKARQKAEKEAR-----LEQEETEKA-LLDLPPVDMETGEILTEEAVQ 266
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                                                                                                                                                                                                                                                                                                                                                           344 LEAT 347
                                                                                                                                                                                                                                                                                                                                                                                          200 FVAT 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36 KDKDEKIEQYDKNVKEQASKDKKQQAKPQIPKDKSKVAGYIEIPDADI-----KEPVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 IAGVVLILVAAYLFAKPHIDNYL-----
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17.2%;
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Pred. No. 2
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CURRENT APPLICATION NUMBER: US/09/196,857A

SARLIER APPLICATION NUMBER: 60/082,418

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/08285440 Patent No. 5532337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 2
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NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                       APPLICATION NUMBER: 07/858,94
FILING DATE: MAICH 27, 1992
ATTORNEY_AGENT INFORMATION:
NAME: WAITEN M. Cheek, Jr.
REGISTRATION NUMBER: 3,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                      INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                              SOFTWARE: DisplayWrite CURRENT APPLICATION DATA: APPLICATION NUMBER: US/
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
MOLECULE TYPE: peptide
                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                CLASSIFICATION: 536 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         255 AKDIDEEVETLADLKEK 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165 TVVID---FVGSIDGVEFD------GGKGENFSLGLGSGQFIPGFEDQ---LVGHSAG 210
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                                STRANDEDNESS:
                                                                                                                                           TELEFAX:
                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 QIPKDKSKVAGYIEIPDADIKEPVYPGPATPEQLNRGVSFAEENESLDDQNISIAGH--- 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Washington
                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                    LENGTH:
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                                                                  558 amino acids
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805 Fifteenth Street, N.W.,
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                                                                                                                                                                                                                            Sequence 6, Application US/08630349 Patent No. 5739008
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Best Local
                                                                                                                                                                                                               GENERAL INFORMATION:
                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
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                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                   APPLICANT: Ken'ichiro HAYASHI et al. TITLE OF INVENTION: POLYPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POSITION IN GENOME:
CHROMOSOME/SEGMENT:
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                                                                                                                                                                       NUMBER OF SEQUENCES:
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IMMEDIATE SOURCE:
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                                                                           CITY: ...
STATE: D.C.
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CELL TYPE:
CELL LINE:
              COMPUTER:
OPERATING
                                                                                                        STREET: 805 Fitte CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                       ZIP:
                                                                                                                                                                                                                                                                                                                                      78 IPDADIKEPVYPGPATPEQLNRGVSFAE---ENESLDDQNISIAGHTFIDRP 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDENTIFICATION METHOD: OTHER INFORMATION:
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 SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS:
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805 Fifteenth Street, N.W.,
             SYSTEM:
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                         IBM Compatible
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25.9%;
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Pred. No.
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CURRENT APPLICATION DATA:

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                                                                              TELEFAX: (415)343-434
INFORMATION FOR SEQ ID NO:
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                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UCBS
TELECOMMUNICATION INFORMATION:
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MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Human Telomerase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              176
                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
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                                                                                                                                                                                                          CLASSIFICATION: 530
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                  STRANDEDNESS:
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not relevant
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Pred. No.
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Best Local Similarity
Matches 35; Conserv
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Best Local
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                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415)343-434;
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: UNITELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 759 amino acids
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NUMBER OF SEQUENCES:
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                                                                227 DMEEEENDDDDDDDDDDEEDGVFDDEDEEEENI----ESKVTKPVQIQKRAVKR----PAPAKS 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                   95
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                                                                                                                                                                                                                                                                           STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: San Francisco
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SDHSEEDSDLEESDSIDDGEELAQSDTSTEEQEDKAVQVSNKKKR-----KLPSDVNEGK 335
                              EQLNRGVSFAEENESLDDQNISIAGHTFIDRPNYQFTNLKAAKKGSMVYFKVGNETRKYK 154
                                                                                                    DKDKDEKIEQYDKNVKEQASKDKKQQAKPQIPKDKSKVAGYIEIPDADIKEPVYPGPATP
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Pred. No. 4.5;
32; Mismatches
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Pred. No. 4.5;
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Best Local Similarity
Matches 35; Conserv
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                                                                    GENERAL INFORMATION:
                                                                                         Sequence 20, Appli
Patent No. 6022739
TITLE
                 APPLICANT: Ryan, Clarence A APPLICANT: Pearce, Gregory L APPLICANT: McGurl, Barry F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (415)343-434 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 759 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: UC
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                    336 TVFIRNLSFDSEEEELGELLQQFGELKYVRIVLHPDTEHSKG 377
                                                                                                                                                                                                                                        155 MTSIR----DVKPTDVGVLDEQKGKDKQLTLITCDDYNEKTG 192
                                                                                                                                                                                                                                                                             281 SDHSEEDSDLEESDSIDDGEELAQSDTSTEEQEDKAVQVSNKKKR-----KLPSDVNEGK 335
                                                                                                                                                                                                                                                                                                                                                 227 DMEEEENDDDDDDDDDEEDGVFDDEDEEEENI----ESKVTKPVQIQKRAVKR----PAPAKS 280
                                                                                                                                                                                                                                                                                                               95 EQLNRGVSFAEENESLDDQNISIAGHTFIDRPNYQFTNLKAAKKGSMVYFKVGNETRKYK 154
                                                                                                                                                                                                                                                                                                                                                                        35 DKDKDEKIEQYDKNVKEQASKDKKQQAKPQIPKDKSKVAGYIEIPDADIKEPVYPGPATP 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
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21.6%;
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; LENGTH: 190
; TYPE: PRT
; ORGANISM: Capsicum annuum
US-08-881-094-20
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Best Local Similarity
Matches 30; Conserv
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EARLIER FILING DATE: 1991-05-24
NUMBER OF SEQ ID NOS: 43
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EARLIER FILING DATE: 1990-05-25
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                                                                                           FILING DATE: Filed H
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
              ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                              SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
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ADDRESSEE: Incyte Ph
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APPLICANT: Hillman, Jennifer.
APPLICANT: Zweiger, Gary B.
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TITLE OF INVENTION: A NOVEL TUMOR PROTEIN
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                                                                               FILING DATE:
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OPERATING SYSTEM:
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                                                                                                                                                            APPLICATION NUMBER:
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  REFERENCE/DOCKET NUMBER:
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3174 Porter Drive
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Goli, Surya K.
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PF-0126 US
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INFORMATION FOR SEQ ID NO: 6:
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APPLICANT:
APPLICANT:
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TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                  SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
               TELECOMMUNICATION INFORMATION:
                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hillman, Jennifer.
APPLICANT: Zweiger, Gary B.
TITLE OF INVENTION: A NOVEL TUMOR PROTEIN
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MOLECULE TYPE:
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                         NAME: Billings, Lucy J.
REGISTRATION.NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0126
                                                                                                                                                                                            OPERATING SYSTEM:
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                                                                                                                                    APPLICATION NUMBER: US/09/162,597 FILING DATE:
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les 43; Conserv
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Pred. No.
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US-08-137-175A-5
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Best Local Similarity
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                                         FILING DATE: 22-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: BARI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
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MOLECULE TYPE:
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TELEPHONE: 202 -- 3528
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STRANDEDNESS: si
                                                                                                                       APPLICATION NUMBER: PCT/US92/08972 FILING DATE: 22-OCT-1992
                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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CLONE: 1072344
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419 Seventh Street, N.W.,
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IMPROVEMENT IN
                                                                                                                                                                                                                                   Release #1.0,
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Pred. No. 1
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; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; TOPOLOGY: Linear
; MOLECULE TYPE: protein
US-08-137-175A-5
Search completed: March 2, 2001, 10:23:05 Job time: 87 sec
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                                                                                       111 SRKVSSKDKTSTDEMFNEKGE-----LSAKTMTRENGTKLEYTEMKSDGTGKAKEVLKN 164
                                                                                                                                                                                   88 YPGPATPEQLNRGVSFAEENESLDDQNISIAGHTFIDRPNYQFTNLKAAKKGS----MVY 143
                                                                                                                                                                                                                                    53 SLKATVDKIELKGTSDKDNGSGVLEGTKDDKSKAKLTIADDLSKTT--FELFKEDGKTLV 110
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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length: 2000000000
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1: /SIDS1/gcgda
2: /SIDS1/gcgda
3: /SIDS1/gcgda
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/SIDS1/gcgdata/geneseq/geneseqp/AA1989.DAT: *
/SIDS1/gcgdata/geneseq/geneseqp/AA1990.DAT: *
/SIDS1/gcgdata/geneseq/geneseqp/AA1991.DAT: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8.2	88.5 8.2 289 19 W55072	8.3 359 19	8.3 161/ 20	00 E 0 3 1617 30 WORULL	0	9 / 55/ 10	8.4 167 18	12.7 223 19	13.6 256 20	14.4 197 20	20	14.9 251 20	Score Match Length DB ID	Query
	2 Streptococcus pneu		Chlamydia pheumoni					Streptococcus pneu	Enterococcus faeca	3 Enterococcus faeca	8 Enterococcus faeca	2 Enterococcus faeca	Description	

New isolated Enterococcus faecalis polynucleotides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus infection

WPI; 1999-070095/06 N-PSDB; X20242.

Bailey C, Choi GH,

Hromockyj A,

Kunsch CA;

ALIGNMENTS

RESULT Y00252 14-NOV-1997; 06-MAY-1997; 16-MAY-1997; Enterococcus faecalis; infection; vaccine; immune response; diagnosis; detection; attenuation; antigenic. 04-MAY-1998; Enterococcus faecalis Enterococcus faecalis protein EF130. Y00252; (HUMA-) HUMAN GENOME SCI INC 12-NOV-1998. WO9850554-A2 20-APR-1999 (first entry) Y00252 standard; Protein; 251 AA 97US-0066009. 97US-0044031. 97US-0046655. 98WO-US08959

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RESULT
Y00158
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Best Local
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                                                                                                                                                         14-NOV-1997;
06-MAY-1997;
16-MAY-1997;
        New isolated Enterococcus faecalis polynucleotides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a protein isolated from Enterococcus faecalis. The present invention describes genes, proteins and antigenic polypeptides isolated from E. faecalis. The proteins can be used in vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal. They can also be used for detecting Enterococcus antibodies in a sample. The nucleotide sequences can be used for detecting Enterococcus nucleic acids.

Products from the present invention can also be used for screening
                                                                 N-PSDB;
                                                                                                      Bailey
                                                                                                                                                                                                                                                                                            Enterococcus
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DB; X20148.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KKWTNRLMTIAGVVLILVAAYLFAKPHIDNYLHDKDKD----EKIEQYD--KNVKEQASK 55
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52; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to identify agonists and antagonists of E. faecalis protein
                                                                                                        Choi
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                                                                                                                                                                                                                                                                                             faecalis
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                                                                                                                                                                                                                                                                                                                                                            faecalis protein EF079
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                                                                                                                                                        97US-0066009.
97US-0044031.
97US-0046655.
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                                                                                                      GH,
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                                                                                                                                 SCI INC
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Pred. No. 6.9e
6; Mismatches
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                                                                                                        Kunsch
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                                                  N-PSDB;
                                                             WPI; 1999-070095/06
                                                                                       Bailey
                                                                                                                                                      14-NOV-1997;
06-MAY-1997;
                                                                                                                                                                                                                                                 WO9850554-A2
                                                                                                                                                                                                                                                                                                    Enterococcus faecalis;
detection; attenuation;
                                                                                                                                                                                                                                                                                                                                           Enterococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 9;
                                                                                                                (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                           16-may-1997;
                                                                                                                                                                                                04-MAY-1998;
                                                                                                                                                                                                                                                                           Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                Y00253;
                                                                                                                                                                                                                                                                                                                                                                                                                        Y00253 standard; Protein; 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                        12-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 ngktlayqvdqiktveptdtkdlhiesgqd-lvtlltctpy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPATPEQLNRGVSFAEENE----SLDDQNISIAGHTFIDRPNYQFTNLKAAKKGSMVYFKV 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lqekmekknqelakkgsnpgldpfsetqkttkkpdksyfeshtigvltipkinvrlpif- 119
                                                                                       c,
                                                  X20243.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      284 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                         faecalis antigenic polypeptide fragment EF130
                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                         97US-0066009.
97US-0044031.
97US-0046655.
                                                                                                                                                                                              98WO-US08959
                                                                                       GH,
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25.3%;
                                                                                       Hromockyj
                                                                                                                                                                                                                                                                                                                infection; vaccine;
                                                                                                                                                                                                                                                                                                    antigenic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -SKDKKQQAKPQIPKDKSKVAGYIEIPDADIKEPVYP 89
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Pred. No. 1.:
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                                                                                       Kunsch CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90;
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New isolated Enterococcus faecalis polynucleotides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus infection

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                    14-NOV-1997;
06-MAY-1997;
16-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents an antigenic polypeptide fragment isolated from Enterococcus faecalis. The present invention describes genes, proteins and antigenic polypeptides isolated from E. faecalis. The proteins can be used in vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal. They can also be used for detecting Enterococcus antibodies in a sample. The nucleotide sequences can be used for detecting Enterococcus nucleic
                                                                                                                                                                                                                                                                                                                                    Enterococcus faecalis;
detection; attenuation;
                         Claim 9; Page 170;
                                                                                                                                                                                                                                    04-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                           Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acids. Products from the present invention can also be used for screening compounds to identify agonists and antagonists of {\rm E.}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                            New isolated Enterococcus faecalis polynucleotides - used products for the detection of Enterococcus and for use in
                                                                                                  N-PSDB; X20149.
                                                                                                                                     Bailey
                                                                                                                                                                                                                                                                                     W09850554-A2
                                                                                                                                                                                                                                                                                                              Enterococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                            Y00159;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                             (HUMA-) HUMAN
                                                                                                                                                                                                                                                             12-NOV-1998
                                               for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 itcgdlgattriavggtlaattpik 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 FIDRPNYQFTNLKAAKKGSMYYFKVGNETRKYKMTSIRDVKPTDVGVLDEQKGKDKQLTL | : |: |: |: :|| |: :||
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les 40; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              kaqfenknlpvigaiaipsveinlpifkglsnvallt-gagtmkedqvmgknnyalashr
                                                                                                            1999-070095/06
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                                                                                                                                   Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             197 AA;
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                                                                                                                                                                                                                                                                                                                                                                        faecalis antigenic polypeptide fragment EF079
                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                              faecalis
                                                                                                                                                             GENOME SCI INC
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97US-0044031.
97US-0046655.
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                     301pp;
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                                                                                                                                   Hromockyj
                                                                                                                                                                                                                                                                                                                                                 infection;
                                                                                                                                                                                                                                                                                                                                     antigenic
                        English
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Pred. No. 1.9e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                 vaccine;
                                                                                                                                     Kunsch CA;
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                                                                                                                                                                                                                                                                                                                                                 immune response; diagnosis;
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                                                 infection
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The present sequence represents an antigenic polypeptide fragment

The present sequence represents a protein from Streptococcus pneumoniae The nucleic acid sequence encoding the Streptococcus pneumoniae protein

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RESULT
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Best Local
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N-PSDB;
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                                                                                                                                                                                                       Nucleic acid encoding antigenic peptide(s) from Streptococcus pneumoniae - or their epitope-containing fragments, useful in protective or therapeutic vaccines, and for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pneumoniae; antigen; vaccine; infection; diagnosis; detection; pneumonia; otitis media; meningitis.
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                                                                                                                          Claim 11; Page 82; 118pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-OCT-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               htigvltipkinvrlpif-dktnalllekgssllegtsyptggtnthavisghrglpgak
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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25.6%; Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Johnson
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Pred. No. 1.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ΑA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kunsch CA;
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RESULT
W89768
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Best Local
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                                                                                                   Barash SC,
Rosen CA;
                                              WPI; 1997-374922/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome;
                                                                                                                                                                                                                                                                                                       07-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                   EP786519-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus protein SEQ ID #5216
                                                                                                                                                                                                                                               05-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
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                                                                                                                                                                                        (HUMA-) HUMAN
                                                                                                                                                                                                                                                                                                                                                               30-JUL-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           {\tt r\text{-}aepshv} f f r h 1 d q 1 k v g d a 1 y y d n g q e i v e y q m d t e i 1 l p s e w e k 1 e s v s s k n - i m t r a e p s h v f f r h 1 d q 1 k v g d a 1 y y d n g q e i v e y q m d t e i 1 l p s e w e k 1 e s v s s k n - i m t r a e p s h v f f r h 1 d q 1 k v g d a 1 y y d n g q e i v e y q m d t e i 1 l p s e w e k 1 e s v s s k n - i m t r a e p s h v f f r h 1 d q 1 k v g d a 1 y y d n g q e i v e y q m d t e i 1 l p s e w e k 1 e s v s s k n - i m t r a e p s h v f f r h 1 d q 1 k v g d a 1 y y d n g q e i v e y q m d t e i 1 l p s e w e k 1 e s v s s k n - i m t r a e p s h v f f r h 1 d q 1 k v g d a 1 y y d n g q e i v e y q m d t e i 1 l p s e w e k 1 e s v s s k n - i m t r a e p s h v f f r h 1 d q 1 k v g d a 1 y y d n g q e i v e y q m d t e i 1 l p s e w e k 1 e s v s s k n - i m t r a e p s h v e f r a e p s e w e k 1 e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s v e s 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TFIDRPNYQFTNLKAAKKGSMVYFKVGNETRKYKMTSIRDVKPTDVGVLDEQKGKDKQLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; Protein; 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                        GENOME
                                                                                                                                                                                                                                               96US-0009861.
                                                                                                                                                                                                                                                                                                       97EP-0100117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.7%;
                                                                                                                                                                                        SCI INC
                                                                                                                                Dillon PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "these residues represent a line of missing te
in the sequence listing in the specification.
They are included to maintain the residue
numbering given in the specification for this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -EKTGVWEK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for inducing protective antibodies against for treatment or prevention of infection e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 137; DB 19;
Pred. No. 1.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                             Fannon MR,
                                                                                                                             Kunsch CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 223;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          text
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В γ

Sequence

167

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identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disk, random access memory (RAM), read-only memory (ROM) or CD ROM. Homology searches using the S.aureus Die Romens allows putative functions to be assigned so that protein encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been industrial and the sequences which are likely to encode antigens have been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polynucleotide(s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of anti-S aureus vaccines
                                                                                                                contained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 23; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ntion. The DNA sequences encoding the S.aureus protein sequence of the computer readable medium, preferably selected from a floppy or hard, random access memory (RAM), read-only memory (ROM) or populations sequence (RAM), read-only memory (ROM) or populations when the computations are recognized to the computations of the computations of the computations are recognized to the computations of the computations are recognized to the computation of t
                                                                                                                                                                        for isolating homologues of any of the 5191 S.aureus DNA sequences
                                                                                                                      on
                                                                                                                      the computer readable medium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3213-3214; 3271pp; English
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Query Match
Best Local S
Matches 40
 Y20763
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                                                                                                                                                                                                                                                                                   5 TNRLMTIAGVVLILVAAYLFAKPHIDNYLHDKDK---DEKIEQYDKNVKEQASKD--KKQ 59
                                                                            sqdksddnqkkt 160
                                                                                                                                                                                                                                                  takvvsiatvllllgglvfaifayvdhsnkakermlneqkqeqkekrqkenaekerkkkq 87
                                                                                                                                     ----grpakeenddkask--
                                                                                                                                                                 HTFIDRPNYQFTNLKAAKKGSMVYFKVGNETRKYKMTSIRDVKPTDVGVLDEQKGKDKQL 179
                                                                                                                                                                                              qeekeqneldsqanqyqqlpqqnqyqyvppqqqaptk--
                                                                                                                                                                                                                            QAKPQIPKDKSKVAGYIEIPDADIKEPVYPGPATPEQLNRGVSFAEENESLDDQNISIAG 119
standard;
                                                                                                                                                                                                                                                                                                                         40;
                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                         Conservative
 Protein;
                                                                                                                                                                                                                                                                                                                                    8.4%; Score 90;
20.8%; Pred. No.
                                                                                                                                                                                                                                                                                                                        30;
                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                    90; DB 18;
No. 0.26;
                                                                                                                                                                                                                                                                                                                      58;
                                                                                                                                                                                                                                                                                                                                                   Length 167
                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                     64;
                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                               124
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QΥ рЬ Š В Š

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RESULT
Y20763
                                                                                                                                                                                                                         frameshift mutation; age-related disease; neurodegenerative disorder; Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal; Huntington's disease; multiple sclerosis; alcoholic liver disease; diabetes mellitus type II; microtubule associated protein; Tau; Big Taubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
                                                                                                        glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;
bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
Synthetic
                                                                                                                                                                                            neurofilament-F; presenilin I; presenilin II; cellular tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human neurofilament-M mutant protein fragment 45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                           beta-amyloid precursor protein; beta-APP; diagnosis;
                                                                           group protein-C;
                                                                           neuroendocrine
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sapiens

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RESULT
W68011
ID W6
XX
AC W6
XX
DT 27
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes a novel method for the diagnosis of a disease C caused by, or associated with, an RNA molecule that has a frameshift c mutation. The method is used to diagnose age-related diseases, especially cancer and a wide range of neurodegenerative disorders (e.g. Alzhelmer's C disease, Down's syndrome, myotonic dystrophy, Huntington's disease, c multiple sclerosis, alcoholic liver disease, diabetes mellitus type II c and many others listed) or susceptibility to these disorders. The method C allows a definitive diagnosis of Alzhelmer's disease in living patients, allows a definitive diagnosis of Alzhelmer's disease in living patients, c at an early stage. It is based on the observation that disease may be c caused by mutations in RNA rather than DNA. The invention describes the used of neuronal system RNA molecules, specifically proteins including beta-amyloid procursor protein (beta-APP), the microtubule associated proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule associated protein 2 (MAP2), neurofilament-I, neurofilament-E, presenilin I, presenilin II, glial fibrillary acidic protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma C (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group on the processor of the company of the
                                                                                                                                                                                                                                                                                                                                                                                                  망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Figure 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; X75759
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(ROYA-)
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   Yeast
                                                                          27-APR-1999
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                                                                                                                                                                                                                   W68011 standard; Protein; 411 AA
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immunophilin FKBP46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39;
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ROYAL NETHERLANDS ACAD
UNIV ROTTERDAM ERASMUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neuroendocrine specific protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 90; DB
Pred. No. 1.4;
26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Van Leeuwen
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W09927105-A2

Chlamydia pneumoniae

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RESULT
Y35617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local 9
Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae. FKBP46 is a novel insect cell nuclear immunophilin, which can be used to study and identify additional immunosuppressive drugs that bind to it. Such immunosuppressive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated immunophilin FKBP46 nucleic acids - useful for developing products for the study and identification of immunosuppressive agents for treating e.g. transplant and tissue graft patients
                                                                               Chlamydia pneumoniae surface exposed polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Column 25-38; 21pp; English.
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31-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunophilin; moth; insect cell; nuclear;
transplant; tissue graft.
                                                                                                                         13-SEP-1999
                                                                                                                                                                                                       Y35617 standard; Protein; 1617
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                                                                                                                                                                                                                                                                                                                                                                                                                           GPATPEQLNRGVSFAEENESLDDQNISIAGHTFIDRPNYQFTNLKAAKKGSMVYFK-VG-
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35; Conserv
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                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA,
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96US-0741134.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred.
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Pred. No. 1;
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tissue graft patients
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Best Local
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           29-JUL-1997;
01-APR-1997;
24-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disease, sarcoidosis, sinusitis, purulent offitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see Y34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
                                                             01-APR-1998;
                                                                                                                                                           GHPO protein;
peptic ulcer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see X91990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart
                                                                                                                                                                                                                         31-MAR-1999
                                                                                                                                                                                                                                                                       W98324 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome sequence of Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-NOV-1998;
21-NOV-1997;
                                                                                     08-OCT-1998
                                                                                                                                    Helicobacter pylori
                                                                                                                                                                                                                                                W98324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 1344-1347; Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-357842/30
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                                                                                                                                                                                                                                                                                                                                                                                   213
                                                                                                                                                                                                                                                                                                                                                                                                                                  153
                                                                                                                                                                                                                                                                                                                                                                                                          99
                                                                                                                                                                                                                                                                                                                                                                                                                                                         49
                                                                                                                                                                                              pylori
                                                                                                                                                                                                                                                                                                                                                           KYKMTSIRDVKPTDVGVLDEQKGKDKQLTLITCDDYNE 189
                                                                                                                                                                                                                                                                                                                                                                                                                                vsekissdtkenrkdletedpskksglkevssdlpkspetavaaisedleisenisardp
                                                                                                                                                                                                                                                                                                                                  ----sdrdivfenl-----vkglsfiscesled 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                        VKEQASKDKKQQAKPQIPKDKSKVAGYIEIPDADIKEPVYPGPATPEQLN------
                                                                                                                                                                                                                                                                                                                                                                              lqglaffykntssqsisekdssfqgiifsgsgansglgfenlkapksgaavy------
                                                                                                                                                                                                                                                                                                                                                                                                -RGVSFAEEN---ESLDDQNISIAGHTFID---RPNYQFTNLKAAKKGSMYYFKVGNETR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
39; Conser
                                                                                                                                                                                                 GHPO
                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                           disease.
                                                                                                                                                                      Helicobacter infection; gastroduodenal disease;
            97US-0902615.
97US-0833457.
97US-0881227.
                                                                                                                                                                                                1411
                                                           98WO-US06371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0107078.
97FR-0014673.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98WO-IB01890.
                                                                                                                                                                                                                                                                       Protein; 359
                                                                                                                                                                                                protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.3%;
24.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 89.5; DI
Pred. No. 7.2;
22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1912pp;
                                                                                                                                                                                                                                                                       AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39;
                                                                                                                                                                        gastritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                212
                                                                                                                                                                                                                                                                                                                                                                                                                                                        98
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RESULT
W55072
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                                                                                                                                                                                                                                                                                                                                                                                 Ωy
                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                   30-OCT-1997;
                                                                                                                                                                                 Streptococcus pneumoniae; antigen; vaccine; inf detection; pneumonia; otitis media; meningitis
                                                                                                                                                                                                                       Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptic ulcer diseases, e.g. gastric and used for the production of antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     these infections, including acute, chronic, and atrophic gastritis, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a Helicobacter pylori GHPO protein of the invention. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroduodenal diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated Helicobacter polynucleotides - for the diagnosis, prevention and treatment infections and gastrointestinal diseases
                                  (HUMA-) HUMAN GENOME SCI INC
                                                           31-OCT-1996;
                                                                                                            07-MAY-1998
                                                                                                                                    WO9818930-A2
                                                                                                                                                           Streptococcus
                                                                                                                                                                                                                                                02-OCT-1998
                                                                                                                                                                                                                                                                                               W55072 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 8; Page 435-437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC. (INMR ) MERIEUX ORAVAX PASTEUR MERIEUX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Al-Garawi A,
                                                                                                                                                                                                                                                                                                                                                            351
                                                                                                                                                                                                                                                                                                                                                                                    152 KYKMTSIRDVK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                   117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        292 vlsrigkahlghvfndgpkelgglrycinsaalrfiplkdmekegygefipyikkg-elk 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                         232 neyynkeeegiyvdittgeplfssadkydsgcgwpsfskpinkdvvkyeddeslnrkrie 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80
                                                                                                                                                                                                                                                                                                                       11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 FAKPHIDNYLHD--KDKDEKIEQYDKNVKEQASKDKKQQAKPQIPKDKSKVAGYIEIP--
                                                                                                                                                                                                                                                                                                                                                           ky----indkk 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1998-542293/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                  ---AGHTFIDRPN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         359 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kleanthous H,
                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                           pneumoniae
                                                                                                                                                                                                                       pneumoniae SP0013 protein
                                                           96US-0029960
                                                                                   97WO-US19422
                                                                                                                                                                                                                                                                                                Protein; 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DADIKEPVYPG------PATPEQLNRGVSFAEENESLDDQNIS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.3%;
25.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2054pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 89;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Miller C,
                                                                                                                                                                                                                                                                                                A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                 -YQFTNLKAAKK---GSMV-YFKVGNETR 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 19;
0.97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SERUMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oomen RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  used to develop
of Helicobacter
                                                                                                                                                                                              infection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tomb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŗ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
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Choi GH,

Hromockyj A,

Johnson LS,

Kunsch CA;

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RESULT
Y30350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qy
 ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               are used to detect Streptococcus infection (by usual hybridisation or amplification methods), also for isolating Streptococcus genes or their allelic variants. The protein can be used similarly to detect specific antibodies in standard immunoassays, especially for diagnosing or monitoring infections. Antibodies which bind the protein are used to detect corresponding antigens, to purify the protein and for passive immunisation (optionally coupled to a toxin). Vaccines are administered, especially at 0.01-1000 corresponding and for through the skin, typically at 0.01-1000 corresponding to the protein are used to the protein and for passive immunisation (optionally coupled to a toxin). Vaccines are administered, one of the protein and for passive that the protein are used to the protein and for passive immunisation (optionally coupled to a toxin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              can be useful in vaccines for inducing protective antibodies against Streptococcus pneumoniae, for treatment or prevention of infection e.g. pneumonia, otitis media or meningitis. Probes based on the nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 19
N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; Page 52; 118pp; English
                                                                                                                                                                                                           W09945121-A1
                                                                                                                                                                                                                                         Streptococcus
                                                                                                                                                                                                                                                                           Pneumoccocal surface adhesion A protein; PsaA; monoclonal antibody; vaccine; Streptococcus pneumoniae infection.
                                                                                                                                                                                                                                                                                                                           37 kDa pneumoccocal
                                                                                                                                                                                                                                                                                                                                                           09-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                           Y30350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pneumoniae - or their epit
protective or therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid encoding antigenic peptide(s) from Streptococcus pneumoniae - or their epitope-containing fragments, useful in
                                Zeiler
                                               Ades EW,
                                                                                                              02-MAR-1998;
                                                                                                                                              26-FEB-1999;
                                                                                                                                                                              10-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                           Y30350 standard; Protein;
                                                                             (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (especially 10-300) mu g/ml per dose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129
                                                                                                                                                                                                                                                                                                                                                                                                                                                          12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 LFAKPHIDNYLHDKDKDEKIEQYDKNVKEQASK----DKKQQAK-PQIPKDK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid sequence encoding the Streptococcus pneumoniae protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mktvsqdtnipiyaqiftd-----siaeqgkegdsyy----smmkynldkiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      afkyfskayg--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ifak-niakqlsakdpnnk-efyeknlkeytdkldkldkeskdkfnkipaekklivtseg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1998-272224/24.
DB; V27333.
1999-540849/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----SKVAGYIEIPDADIKEPVYPGPATPEQLNRGVS-----FAEENESLDDQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----NISIAGHTFIDRPNYQFTNLKAAKKGSMVYFKVGNETRKYKMTSIRD 160
                                               Carlone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        289 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence represents a protein from Streptococcus
                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                           pneumoniae
                                                                                                              98US-0076565
                                                                                                                                              99WO-US04326
                                               GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ·vpsayiweinteeegtpeqiktlveklrqtkvpslfve--ssvddrp
                                                                                                                                                                                                                                                                                                                           surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.2%;
28.0%;
                                                                                                                                                                                                                                                                         pneumoniae
                                               Sampson
                                                                                                                                                                                                                                                                                                                                                                                                                           309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vaccines,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18;
                                                                                                                                                                                                                                                                                                                         adhesion A protein (PsaA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 88.5;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                          A
                                               JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and
                                            Tharpe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
                                             JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
                                             Westerink
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11;
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RESULT 13
W82496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DR PT PT SXX
Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                      17-SEP-1996;
17-SEP-1991;
04-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a pneumoccocal surface adhesion A pro (PsaA). The specification describes monoclonal antibodies which bind epitopes of the PsaA protein (see Y30351-54). These peptides can be used in vaccines to prevent Streptococcus pneumoniae infections. The antibodies of the invention can also be used to detect S. pneumoniae a sample or individual.
                                        Nucleic acid encoding the 37 kDa. surface adhesion A of pneumoniae - useful diagnostically and for production c
                                                                                                                                                                                                                                                                                                                          S. pneumoniae
                                                                                                                                                                                                                                                                                                                                                                      W82496;
                                                                                                                                                                                                                                                                                                                                                                                           W82496 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New peptides for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; Z10411.
                                                                            N-PSDB;
                                                                                                             Ades EW,
                                                                                                                                                                                                   17-SEP-1996;
                                                                                                                                                                                                                         29-DEC-1998
                                                                                                                                                                                                                                               US5854416-A
                                                                                                                                                                                                                                                                    Streptococcus
                                                                                                                                                                                                                                                                                          diagnostic;
                                                                                                                                                                                                                                                                                                    Surface adhesion A protein;
                                                                                                                                                                                                                                                                                                                                                04-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  subject
                               recombinant polypeptides
                                                                                                                                  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   262 mktvsqdtnipiyaqiftd-----siaeqgkegdsyy----smmkynldkiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 -----SKVAGYIEIPDADIKEPVYPGPATPEQLNRGVS------FAEENESLDDQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 LFAKPHIDNYLHDKDKDEKIEQYDKNVKEQASK----DKKQQAK-PQIPKDK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
mes 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             afkyfskayg---vpsayiweinteeegtpeqiktlveklrqtkvpslfve--ssvddrp
                                                                                       1999-095007/08
                                                                           V73914.
                                                                                                             Carlone GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 53-54; 58pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          309 AA;
                                                                                                                                                                                                                                                                                        immunoassay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -NISIAGHTFIDRPNYQFTNLKAAKKGSMVYFKVGNETRKYKMTSIRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           corresponding or preventing
                                                                                                                                                                                                                                                                                                                        37-kDa surface adhesion A protein
                                                                                                                                                                                                                                                                    pneumoniae
                                                                                                                                                      96US-0715131.
91US-0791377.
94US-0222179.
                                                                                                                                                                                                   96US-0715131
                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.2%;
                                                                                                             Russell
                                                                                                                                                                                                                                                                                          treatment;
                                                                                                                                                                                                                                                                                                                                                                                            309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to Streptococcus pneumoniae PsaA, streptococcus pneumoniae infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18;
                                                                                                                                                                                                                                                                                                    vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 88.5; DB Pred. No. 0.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English.
                                                                                                                                                                                                                                                                                                                                                                                            AA
                                                                                                             Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                          Sampson
                                                                                                                                                                                                                                                                                        detection; serotype; antibody;
infection; anti-idiotype.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BB
                                                                                                             JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53;
                                                                                                           Tharpe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                          f Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        used
                                                                                                                                                                                                                                                                                                                                                                                                                                                  305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
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Claim 1; Column 33-34; 20pp; English

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RESULT 14
Y81668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents a Streptococcus pneumoniae 37-kDa surface adhesion A protein. This encoding nucleic acid can be used in methods to express recombinant protein, as a source of primers for amplification (to identify and isolate related sequences, e.g. alleleic variants) or probes for nucleic acid hybridisation tests for detecting S. pneumoniae, and in DNA vaccines. This protein and its fragments can be used to raise antibodies, in vaccines and for detecting S. pneumoniae (by reaction with specific antibodies). Antibodies are useful in diagnostic immunoassays, to treat infections and to raise anti-idiotype antibodies for use in vaccines. This protein is very highly conserved between the different serotypes of S. pneumoniae so is an excellent candidate for vaccine
                                                                                                               New Streptococcal protein, useru
pneumococcal diseases and for sc
isolated from specifically (
                                                                                                                                                                                                                                                                                                                            27-JUL-1998;
19-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pneumoniae protein sequence ID205
                                                                                 Claim
                                                                                                                                                                                                       WPI; 2000-195300/17
                                                                                                                                                                                                                                            Gilbert CFG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pneumococcal disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                  (MICR-) MICROBIAL TECHNICS
                                                                                                                                                                                                                                                                                                                                                                                                                               10-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y81668 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               development.
                                                                                                                                                                                                                                                                                                                                                                                       27-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 LFAKPHIDNYLHDKDKDEKIEQYDKNVKEQASK----DKKQQAK-PQIPKDK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mktvsqdtnipiyaqiftd---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     afkyfskayg---vpsayiweinteeegtpeqiktlveklrqtkvpslfve--ssvddrp
to Y81679 represent specifically claimed protein sequences ed from Streptococcus pneumoniae. A05407 to A05590 represen ically claimed nucleotide sequences isolated from S. pneumo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49;
                                                                               Page 90; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -SKVAGYIEIPDADIKEPVYPGPATPEQLNRGVS-----FAEENESLDDQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       309
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                                                                                                                                                                                                                                            Hansbro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pneumoniae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                                                                                            98GB-0016337
99US-0125164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.2%;
28.0%;
                                                                                                                                                                                                                                               PM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         310
                                                                                                                                                             useful as a vaccine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 88.5; DB Pred. No. 0.88;
                                                                                                                     he protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -siaeqgkegdsyy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       meningitis;
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                                                                                                                                        of antagonizing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosis;
                       represent
pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55;
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Best Local S
Matches 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequences have antibacterial and antiinflammatory properties. The protein sequences, and fragments of them, are useful as immunogens and/or antigens. The nucleotide sequences can be useful for the diagnostic assays. The proteins and nucleotides can be useful for the detection and diagnosis of S. pneumoniae. The protein sequences are also useful for screening an agent capable of antagonising, inhibiting or interfering with the function or expression of the proteins in which the agent is useful for treatment or prophylaxis of S. pneumoniae infection and meningitis. A05591 to A05614 represent primers used in the exemplification of the present invention.
The present sequence represents an antigenic polypeptide fragment isolated from Enterococcus facealis. The present invention descrigenes, proteins and antigenic polypeptides isolated from E. facea The proteins can be used in vaccines for preventing or attenuation.
                                                                                               New isolated Enterococcus faecalis polynucleotides - used products for the detection of Enterococcus and for use in for prevention or attenuation of Enterococcus infection
                                                                                                                                                                                                                                                                         14-NOV-1997;
06-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Y00215 standard;
                                                                      Claim
                                                                                                                                                         N-PSDB;
                                                                                                                                                                      WPI; 1999-070095/06
                                                                                                                                                                                                   Bailey
                                                                                                                                                                                                                              (HUMA-) HUMAN
                                                                                                                                                                                                                                                           16-MAY-1997;
                                                                                                                                                                                                                                                                                                                   04-MAY-1998;
                                                                                                                                                                                                                                                                                                                                               12-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                        Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                    detection; attenuation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enterococcus faecalis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262 mktvsqdtnipiyaqiftd-----siaeqgkegdsyy-----smmkynldkiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           207 afkyfskayg---vpsayiweinteeegtpeqiktlveklrqtkvpslfve--ssvddrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 LFAKPHIDNYLHDKDKDEKIEQYDKNVKEQASK----DKKQQAK-PQIPKDK------
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                                                                      9;
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                                                                                                                                                         x20205
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                                                                      Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   310 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           faecalis antigenic polypeptide fragment EF106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first
                                                                      205;
                                                                                                                                                                                                                               GENOME
                                                                                                                                                                                                                                                        97US-0066009.
97US-0044031.
97US-0046655.
                                                                                                                                                                                                                                                                                                                 98WO-US08959
                                                                                                                                                                                                 GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein; 310
                                                                   301pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.2%;
                                                                                                                                                                                                                               SCI INC
                                                                                                                                                                                                 Hromockyj.A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                infection; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                  antigenic
                                                                    English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 88.5;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA
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                                                                                                                                                                                                   Kunsch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                immune response;
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                                                                                                               vaccines
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                          describes
                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnosis;
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CC infection caused by a member of the Enterococcus genus in an animal.

CC They can also be used for detecting Enterococcus antibodies in a sample.

CC The nucleotide sequences can be used for detecting Enterococcus nucleic cc acids. Products from the present invention can also be used for CC screening compounds to identify agonists and antagonists of E. faecalis cc protein activity.

XX SQ Sequence 310 AA;

Query Match 8.1%; Score 87; DB 20; Length 310; Best Local Similarity 25.7%; Pred. No. 1.2; Matches 28; Conservative 20; Mismatches 35; Indels 26; Gaps 5; Matches 28; Conservative 20; Mismatches 35; Indels 26; Gaps 5; Matches 28; Conservative 20; Mismatches 35; Indels 26; Gaps 5; Matches 28; Conservative 30; Mismatches 35; Indels 26; Gaps 5; Matches 28; Conservative 30; Mismatches 35; Indels 26; Gaps 5; Matches 28; Conservative 30; Mismatches 35; Indels 26; Gaps 5; Matches 28; Conservative 30; Mismatches 35; Indels 26; Gaps 5; Matches 28; Conservative 30; Mismatches 35; Indels 26; Gaps 5; Matches 28; Conservative 30; Mismatches 35; Indels 26; Gaps 5; Matches 28; Conservative 30; Mismatches 35; Indels 26; Gaps 5; Matches 36; Indels 26; Gaps 5; Matches 28; Indels 26; Gaps 5; Matches 36; Indels 26; Indels
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OM nucleic -
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Copyright (c) 1993 - 2000 Comp
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US-08-082-849B-7
PCT-US94-01624-7
US-08-081-849B-9
PCT-US94-01624-9
US-08-081-601-9
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6.2	6.2	6.2	6.2	6.2	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.5	6.5	6.5	6.5
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Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 169, App	Sequence 169, App	Sequence 4, Appli	Sequence 1, Appli	Sequence 6, Appli	Sequence 8, Appli	Sequence 7, Appli	Sequence 14, Appl	Sequence 13, Appl	-		25,	Sequence 1342, Ap	Sequence 1, Appli

ALIGNMENTS

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US-08-232-463-14
                                                                                                                                                            APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMM
REFERENCE/TOCKET NUMBER: 30472/114 IMM
TELECOMMUNICATION INFORMATION:
TELEFAN: (703)683-409
TELEFAN: (703)683-419
INFORMATION FOR SEQ ID NO: 14:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: DORNER, F. APPLICANT: SCHEIFLINGER, F. APPLICANT: FALKNER, F. G. TITLE OF INVENTION: RECOMBINANT NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                IMMEDIATE SOURCE:
CLONE: pTZgpt-
                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pair
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PRIOR APPLICATION DATA:
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CITY: Alexandria
STATE: VA
COUNTRY: USA
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TOPOLOGY: lir
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Best Local Similarity
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 18-SEP-198
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                                                                                     312 agaagaaaatgaatcactagatgatcaaaatatttcaattgcaggacacactttcattga 371
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Patent No.
                                Query Match
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Matches 230; Conserv
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APPLICANT: Williamson, Kim (
APPLICANT: Kaslow, David C.
                                                                                                                                                                                                                                                                                   TELEFAX: (415)
INFORMATION FOR SEQ
                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/0 FILING DATE: 13-OCT-1994 CLASSIFICATION: 424 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 0
FILING DATE: 29-JAN-1993
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                   FEATURE:
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CITY: S
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84 tatcgataattatcttcacgataaagataaagatgaaaagattgaacaatatgataaaaa 143
                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                   NAME: Quine, Jonathan REGISTRATION NUMBER: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Francisco
STATE: California
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                               Score 50.6; DB 1;
Pred. No. 0.0014;
0; Mismatches 299;
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                                                               Length 9636;
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                                  INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                  SEQUENCE CHARACTERISTICS:
                                                                                                                                     CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                               SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Delencastre, Herminia
TITLE OF INVENTION: AUXILIARY GENES AND PROTEINS
TITLE OF INVENTION: METHICILLIN RESISTANT BACTERI
                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                          NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600
                                                TELEFAX:
                                                                                                                                                                   APPLICATION NUMBER: US/0 FILING DATE: 10-JUL-1996
                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                             TELEPHONE:
                                                                                                                          NAME:
                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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                                                             201-487-5800
   pairs
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                                                          CORRESPONDENCE ADDRESS:
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STREET:
CITY: A
STATE:
                                           ADDRESSEE:
              Atlanta
                          E: Needle & Rosenberg, P.C. 133 Carnegie Way, Suite 400
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Matches 199;
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Best Local Similarity
                                                                                                                                         GENERAL INFORMATION: APPLICANT: Leppla
APPLICANT: Arora, Naveen
APPLICANT: Singh, Vegendra
TITLE OF INVENTION: ANTHRAX TOXIN FUSION PROTEINS
TITLE OF INVENTION: RELATED METHODS
NUMBER OF SEQUENCES: 12
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LOCATION:
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                                                                                                                                                                                                      Application US/08021601
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                                                                                                Leppla, Stephen H. Klimpel, Kurt R. Nichols, Peter J.
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Pred. No. 0.0038;
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Nichols, Peter J.

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                                                                      Sequence 5, Application US/08082849B Patent No. 5677274 GENERAL INFORMATION:
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Best Local
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 APPLICANT:
                                     APPLICANT:
APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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Local Similarity 44.9%;
hes 182; Conservative
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Arora,
Singh,
                                   Leppla, Stephen H
Klimpel, Kurt R.
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UMBER: 36,016
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Pred. No. 0.0032;
0; Mismatches 223;
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; OTHER INFORMATION:
US-08-082-8498-5
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Best Local Similarity
Matches 182; Conserva
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ANTI-SENSE: NO
ORIGINAL SOURCE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 0: FILING DATE: 12-FEB-1993 ATTORNEY/AGENT INFORMATION: Weber, Kenneth A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
TITLE OF INVENTION:
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406 gccaaaaaaggtagtatggtgtactttaaagttggtaatgaaacacgtaagtataaaatg 465
                                       361 GCAAAAGAAGGATATGAACCCGTACTTGTAATCCAATCTTCGGAAGATTATGTAGAAAAT
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44.9%;
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PCT-US94-01624-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
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TITLE OF INVENTION: ANTHRAX TOXIN FUSION PROTEINS AND TITLE OF INVENTION: RELATED METHODS
                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                              TOPOLOGIE TYPE: DN
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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166 gataaaaagcagcaagctaaacctcaaattccgaaagataaatcgaaagtggcaggctat 225
                                                   121 AAACACATTGTAAAAATAGAAGTAAAAGGGGGAGGGAAGCTGTTAAAAAAAGAGGCAGCAGAA 180
                                                                   106 aaagattaaagattgaaaagattgaacaatatgataaaaatgtaaaagaacaggcgagtaaa 165
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                                                                                                                                                                                                                           LOCATION: 1..1368
OTHER INFORMATION:
OTHER INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                               ORGANISM:
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Singh, Yogendra
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                                                                                                                       Conservative
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"LF(1-254)--TR--PE(401-602)"
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                                                                                                                   TELEFAX: 404/000 7:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
SEQUENCE TENGTH: .1425 base pairs
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GENERAL INFORMATION:
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                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                 CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Spratt, Gwendolyn
                                                   MOLECULE TYPE: FEATURE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                             NAME: Spratt, Gwendolyn D
REGISTRATION NUMBER: 36,0
                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US FILING DATE: 19930212
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ZIP: 30303
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                                    NAME/KEY:
                                                                                      TOPOLOGY:
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133 Carnegie Way, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Klimpel, Kurt R. Nichols, Peter J.
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Singh, Yogendra
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                 TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                   NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 15:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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SEQUENCE
                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                  CLASSIFICATION: 514
PRIOR APPLICATION DATA:
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                                                  TELEPHONE:
                                                                                                                                                              APPLICATION NUMBER: US 0 FILING DATE: 12-FEB-1993
                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0: FILING DATE: 25-JUN-1993
                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
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nes 182; Conservative
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CHARACTERISTICS:
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Singh, Yogendra
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O Embarcadero Center, Eighth
                                                     (415)
                                                    576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anthrax Toxin Fusion Proteins and Related Methods
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                                                                                                                                                                                   US 08/021,601
                                                                                                                                                                                                                                                        US/08/082,849B
                                                                                        15280-161-1
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smatches 223;
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PCT-US94-01624-7
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; OTHER INFORMATION:
US-08-082-849B-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local Similarity
               Alt: ALTERNATION OF THE PROPERTY OF THE PROPER
                                                                                                                                                                                                                                                                                        CORRESPONDENCE: TOWNSEND and TOWNSEND KHOURIE and ADDRESSEE: TOWNSEND and TOWNSEND KHOURIE and
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Nichols, Peter J.
TITLE OF INVENTION: ANTHRAX TOXIN FUSION PROTEINS
TITLE OF INVENTION: RELATED METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL: NO ORIGINAL SOURCE:
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MOLECULE TYPE: DN
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                                                                                                                                                                                                                                            CITY: San Francisco
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      SOFTWARE:
                                                                                                                                                                                  COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCAAAAGAAGGATATGAACCCGTACTTGTAATCCAATCTTCGGAAGATTATGTAGAAAAT
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                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arora, Naveen
Singh, Yogendra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Klimpel,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leppla, Stephen Н.
   PatentIn
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44.9%;
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Release #1.0,
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Version
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Sequence 9, Application US/08021601
Patent No. 5591631
GENERAL INFORMATION:
APPLICANT: Leppla, Stephen H.
APPLICANT: Klimpel, Kurt R.
APPLICANT: Nichols, Peter J.
APPLICANT: Arora, Naveen
APPLICANT: Singh, Yogendra
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Best Local Similarity 44.9
Matches 182; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 15:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
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ORIGINAL SOURCE:
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APPLICATION NUMBER: PC
FILING DATE: June 25,
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
 TITLE
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LOCATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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 NT: Arora, N
NT: Singh, Y
F INVENTION:
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ANTHRAX TOXIN FUSION PROTEINS
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"LF(1-254)--TR--PE(398-613)"
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Pred. No. 0.0032;
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US-08-021-601-9
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Best Local Similarity
Matches 182; Conserv
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NAME: Spratt, Gwendolyn D.
REGISTRATION NUMBER: 36,016
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CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
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STATE:
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CLASSIFICATION:
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SOFTWARE: PatentI
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FILING DATE: 19930212
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                         acaagtataagagatgttaagcctacagatgtaggagttctagat 510
                                                        ACTGAAAAGGCACTGAACGTTTATTATGAAATAGGTAAGATATTATCAAGGGATATTTTA
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Y: USA
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 0.0033;
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RESULT 12 US-08-082-849B-9

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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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                            286 caattaaatagaggtgtaagctttgcagaagaaaatgaatcactagatgatcaaaatatt 345
                                                                                          226 attgaaattccagatgctgatattaaagaaccagtatatccaggaccagcaacacctgaa
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                                                                                                                                                                                            121 AAACACATTGTAAAAATAGAAGTAAAAGGGGGAGGAAGCTGTTAAAAAAGAGGCAGCAGAA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
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Pred. No. 0.0033;
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RESULT 13
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION: NAME: Weber, Kenneth A.
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                                                                                                                                                           FEATURE:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 543-9600
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                                                                                            LOCATION: 1..1524
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                         NAME/KEY:
                                                                                                                                                                         ORGANISM:
                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                    STRANDEDNESS
                                                                                                                                                                                                                                                                     TYPE:
                                                                                                                                                                                                                                                                                                                                   TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: POFILING DATE: June 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
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Singh, Yogendra
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Klimpel, Kurt R.
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"LF(1-254)--TR--PE(362-613)"
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Score 48.2; DB 4; Length 1524; Pred. No. 0.0033; 0; Mismatches 223; Indels 0
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                                                                                                                                TELEFAX: 404/688-9880
NFORMATION FOR SEQ ID NO:
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APPLICANT:
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                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 3291 base pairs
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CORRESPONDENCE ADDRESS:
               ORIGINAL
                                 MOLECULE TYPE:
                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                      CLASSIFICATION:
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                                               TOPOLOGY:
                                                             STRANDEDNESS:
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               SOURCE:
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133 Carnegie Way, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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Singh, Yogendra
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Bacillus anthracis
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; NAME/KEY:
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US-08-021-601-1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                  APPLICANT: Singh, YO
APPLICANT: Nichols,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/021,601
FILING DATE: 12-FEB-1993
                                                                                                           CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: Townsend and Townsend and Crew LLF
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                                                           CLASSIFICATION:
                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                           ZIP:
                                                                                                                                                                                                                                                         CITY:
                                                                             FILING DATE:
                                                                                           APPLICATION NUMBER:
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California
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                                                                                                                                                                                                                                                                                                                                                                                                                             Leppla, Stephen H.
                                                                                                                                       IBM PC compatible SYSTEM: PC-DOS/MS-DOS
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                                                                          25-JUN-1993
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                                                                                           US/08/082,849B
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                                                                                                                                                                                                                                                                                                                                                 Toxin Fusion Proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; FEATURE:
; NAME/KEY: CDS
; LOCATION: 580..2907
; OTHER INFORMATION: /product= "Lethal Factor"
US-08-082-849B-1
В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.8%;
Best Local Similarity 44.9%;
Matches 182; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bacillus anthracis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
(INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3291 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 31,677
REFERENCE/FOCKET NUMBER: 15:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
1060 AGTAAAATTAATCAACCATATCAGAAATTTTTAGATGTATTAAAT 1104
                                                                                  1000 ACTGAAAAGGCACTGAACGTTTATTATGAAATAGGTAAGATATTATCAAGGGATATTTTA 1059
                        466 acaagtataagagatgttaagcctacagatgtaggagttctagat 510
                                                                                                                                                                                                                                                                                                                                        406 gccaaaaaaggtagtattggtgtactttaaagttggtaatgaaacacgtaagtataaaatg 465
                                                                                                                                                                    940 GCAAAAGAAGGATATGAACCCGTACTTGTAATCCAATCTTCGGAAGATTATGTAGAAAAT 999
                                                                                                                                                                                                 346 tcaattgcaggacacctttcattgaccgtccgaactatcaattttacaaatcttaaagca 405
                                                                                                                                                                                                                                                      880 AAGAAAAAAATAAAAGACATTTATGGGAAAGATGCTTTATTACATGAACATTATGTATAT 939
                                                                                                                                                                                                                                                                            286 caattaaatagaggtgtaagctttgcagaagaaaatgaatcactagatgatcaaaatatt 345
                                                                                                                                                                                                                                                                                                                                                                                                                               760 AAGCTACTTGAGAAAGTACCATCTGATGTTTTAGAGATGTATAAAGCAATTGGAGGAAAG 819
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              700 AAACACATTGTAAAAATAGAAGTAAAAAGGGGAGGAAGCTGTTAAAAAAAGAGGCAGCAGAA 759
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Pred. No. 0.004;
0; Mismatches 223;
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Search completed: March 14, 2001, 14:28:04 Job time: 27600 sec

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Scoring table:
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database :
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
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621
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Copyright (c) 1993 - 2000 Compugen Ltd.
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predicted score of 1																			-															

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

იი	Result No.	Score 621 340.2 315.2	% Query Match 100.0 54.8 50.8		DB 1	ID AF162687 AF269739 AF269386
	ω	315.2 72.4		4017 152409	84	AF269386 PFMAL1P1
O	თთ	68 67.2	11.0 10.8	196490 2069	29 21	AC005507 E10125
	o 8 7	66.8	10.8	3399 1686	21	E10126 E08995
C	10	66.4	. 7	1324	560	PFRESAR1
	11	66.4	10.7	4591	81	A00661
a	12	65.4	10.5	7218	81	166494
	13	64.4	10.4	12029	31	AE001373
O	14	64.2	10.3	201289	49	AC021008
a	15	64	10.3	879	79	CNS01JRG
ဂ	16	64	10.3	51014	39	AC011856
O	17	63	10.1	143585	39	AC013349
	18	62.8	10.1	5420	32	AF056936
C	19	62.4	10.0	202748	84	CNS05TEB
O	20	62	10.0	83440	51	AC024285
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AF162687
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                                                                                                                                                              source
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Staphylococcus a
AF162687
                                                                                                                                                                      Direct Submission
Submitted (24-JUN-1999) Microbiology
Conte Avenue, Los Angeles, CA 90095,
                                                                                                                                                                                                                             Staphylococcus aureus sortase, an enzyme that anchors surface proteins to the cell wall Science 285 (5428), 760-763 (1999) 99357874
                                                                                                                                                                                                     2 (bases 1 to 1256)
Mazmanian, S.K., Liu,
                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillus/Clostridium group; Bacilus/Staphylococcus group; Staphylococcus. 1 (bases 1 to 1256)
Mazmanian,S.K., Liu,G., Ton-That,H. and Schneewin
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                             /product-"sortase"
/protein_id-"aad48437.1"
/d_xref-"GI-"5726436"
/tanslation-"MKKWTNRLMTIAGVVLILVAAYLFAKPHIDNYLHDKDKDEKIEQ
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FAEENESLDDQNISIAGHTFIDRPNYQFTNLKAAKKGSMVYFKVGNETRKYKMTSIRD
              VKPTDVGVLDEQKGKDKQLTLITCDDYNEKTGVWEKRKIFVATEVK"
185 c 234 g 367 t
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                                                                                                                                             /organism="Staphylococcus
/strain="8325-4"
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825
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                                                                                               /note="transpeptidase"
                                                                                                                                                                     Location/Qualifiers
                                                                               transl_table=11/
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                                                                                                       /gene="srtA"
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AL110675 Botrytis
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AC022680 Homo sapi
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AC034105 Homo sapi
AC032851 Homo sapi
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Staphylococcus
                      genome
                             Transposon-mediated
                                                                             Bacillus/Staphylococcus group;
1 (bases 1 to 2356)
                                       Furdon,P.J.
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      င်
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atgaaaaaatggacaaatcgattaatgacaatcgctggtgtggtacttatcctagtggca
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Staphylococcus epidermidis
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                            Kimmerly, W.J., Taylor, J.David, Nelsen, A.J., Godlevski, M. Rubino, M.A., Nelson, F.J., Rivers, P.R., Torruella Miller, Listenbee, S., Ashanti, C., Altshuller, G., Mamo, L., Shephe Fuchs, R., Fleming, T., Guan, X., Du, L., Cain, D.H., Miller,
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AF269386 40:
Staphylococcus (
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Drive, Research Triangle Park, North Carolina 27709-3398, USA
Location/Qualifiers
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Direct Submission
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/strain="SR1"
/db_xref="taxon:1282"
/clone="step.1020h12"
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Submitted (19-MAY-2000) Departments of Genomic Sciences and
Bioinformatics, Genetics Directorate, Glaxo Wellcome, Inc., 5
Drive, Research Triangle Park, North Carolina 27709-3398, USA
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Taylor, J. David, Kimmerly, W.J., Nelsen, A.J., Godlevski, M.M., Rubino, M.A., Nelson, F.J., Rivers, P.R., Torruella-Miller, I., Listenbee, S., Ashanti, C., Altshuller, G., Mamo, L., Shepherd, Fuchs, R., Fleming, T., Guan, X., Du, L., Cain, D.H., Miller, G.S.
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/strain="SR1"
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Pred. No. 6.1e-41;
0; Mismatches 128;
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On Aug 12,
For more in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Order of segments is not known; 800 n's separate segments.
* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and Barrell, B.
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1 (bases 1 to 152409)
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malaria parasite P. falciparum.
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Pred. No. 0.0043;
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94304, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Aug 12, 2000 this sequence version replaced gi:8810456.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                       * arbitrary. Gaps between the contigs are represented as truns of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence truncated as the sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (21-AUG-1998) Stanford
Center, Stanford University, 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hyman,R.W., Fung,E.L., Qin,F., Rowley,D., Mao,J., Kurdi,O.B., Conway,A.B. and Davis,R.W. Plasmodium falciparum 3D7 chromosome 12
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Eukaryota; Alveolata; Apicomplexa;
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Hyman, R.W., Qin, F., Fung, E.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
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/clone="3D7"
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/db_xref="taxon:5833"
/chromosome="12"
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atcgaaagtggcaggctatattgaaattccagatgct 243
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[1-2069]

Doi H., Nagakuchi Y., Tanaka Y., Fujisaki Y.;
Doi H., Nagakuchi Y., Tanaka Y., Fujisaki Y.;
"GENE CLONE MANIFESTING CHICKEN LEUCOCYTOZOON IMMUNOGENIC RECCOMBINANT VACCINE AGAINST CHICKEN LEUCOCYTOZOON";
Patent number JP1995284392-A/1, 31-CCT-1995.

DOUBUTSUYOU SEIBUTSUGAKUTEKI SEIZAI KYOKAI, KITASATO INST.
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        unidentified unclassified
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                                                                                                                                                      JP 1995284392-A/1
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               misc_feature
                                misc_feature
                                                misc_feature
                                                                           source
                                                                                           Key
                                                                                                   topology:
                                                                                                                                               31-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                        standard;
                                                                                                   Linear;
                                                                                                                                                                                                                                                                                                             65,
                                                                                                                                                                                                                                                                                                                                                                        RNA;
      2045. .2069
/note="EcoRI adaptor"
25. .2046
/product="immunogenicity
                                                /organism="Leucocytozon/strain="shizuoka"
1...25
                                        /note="EcoRI
                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                            Created)
Last updated,
                                                                                                                                                                                                                                                                                                                                                                        UNC;
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       protein"
                                                                                                                             FUJISAKI YUJIRO
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Best Local Similarity
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                                                                                                              DNA encoding an maltose-binding
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DOI H., Nagakuchi Y., Tanaka Y., "GENE CLONE MANIFESTING CHICKEN
                                                        unidentified unclassified
                                                                                           JP 1995284392-A/2
                                                                                                                                                 08-OCT-1997
02-SEP-2000
                                                                                                                                                                                     E10126.1
                                                                                                                                                                                                           E10126;
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                                                                                                               protein.
                                                                                                                          immunogenicity
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Last upd
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, Fujisaki Y.;
LEUCOCYTOZOON
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                                                                                                                                                                                                                                 ВР
                                                                                                                          of Leucocytozon
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IMMUNOGENIC PROTEIN AND GENE

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Query Match
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DOUBUTSUYOU SEIBUTSUGAKUTEKI SEIZAI KYOKAI, KITASATO
 2429
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              aagcagccaaaaaaggtagtatggtactttaaagttggtaatgaaacacgtaagtata
                                                                                                                                                                        ctgaacaattaaatagaggtgtaagctttgcagaagaaaatgaatcactagatgatcaaa
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                                                   AAGAAGAAGTAACACATGAAGAAGAAAAAGAAGAAGTAACACATGAAGAAGAAAAAAGAAG
                                                                                                                              atatttcaattgcaggacacactttcattgaccgtccgaactatcaatttacaaatctta
                                                                                                                                                         ATGAAGAAGAAGAAAAAAGTAATACATGAAGAAGAAAAAAGAAGAAGTAATACATGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Artificial sequences.
JP 1995284392-A/2
31-OCT-1995
19-APR-1994 JP 1994080643
AAGTAACACGTGAAGAAGAAGAAAAAGTAACACATGAAGAAGAAAAAAGAAGTAACAC
                                                                                                     AAGAAAAAGAAGAAGTAACACATGAAGAAGAAGAAAGAAGAAGTAACACATGAAGAAGAAA
                                                                                                                                                                                                                                                                                       gtaaagataaaaagcagcaagctaaacctcaaattccgaaagataaatcgaaagtggcag
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                                                                                                                                                                                                                                                                                                                                                                                                                                   3399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="unidentified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                                                                                                 1577 A; 509 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.3218
/note="ECORI adaptor"
3219, .3399
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3194..3
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1174. 3195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="maltose-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mmunogenicity protein"
                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunogenicity
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                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                          Matches
                                                                 Query Match
Best Local
                                                                                                                                                                    Kato A., Onaga H., Ueda S.;
"POLYPEPTIDE INDUCING IMMUNITY AGAINST LEUCOCYTOZOON
RECOMBINANT DNA MOLECULE CODING THE POLYPEPTIDE";
Patent number JP1995089995-A/1, 04-APR-1995
                                                                                                                                                                                                                                                                                                                                                                 [1]
1-1686
                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA
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02-SEP-2000
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                                                                                                  Sequence
                                                                                                                                   source
                                                                                                                                                  Key
                                                                                                                                                                                                                                                                                                                         DOUBUTSUYOU SEIBUTSUGAKUTEKI SEIZAI KYOKAI,
                                                                                                                                                                                                                                                                                                                                                                                          unidentified unclassified
                                                                                                                                                                                                                                                                                                                                                                                                                  JP 1995089995-A/1.
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ataaaaatgtaaaagaacaggcgagtaaagataaaaagcagcaagctaaacctcaaattc
                                  aaccacatatcgataattatcttcacgataaagataaagatgaaaagattgaacaatatg
                                                                                                                                                                                                                                                                10-SEP-1993 JP 1993226078
KATO ATSUSHI, ONAGA HIROSUKE,
C07K14/44,A61K39/015,C12N1/21
                                                                                                                                                                                                                                                                                         Leucocytozoon caulleryi
JP 1995089995-A/1
04-APR-1995
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                         mat_peptide
                                                                                                                                                                                                          source
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Submitted (17 NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 13, 2000 this sequence version replaced gi:6939328.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                            Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morman, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morman, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Myman, D., Ye, M. J., Zimmer, A. and Zody, M.
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contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone
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23638: contig of 940 bp
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27865:

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2 44336: contig of 9
7 44436: gap of 10
7 45355: contig of 9
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48460: contig of 936 bp
4850: gap of 100 bp
49507: contig of 947 bp
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64986: contig of
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56781: contig of
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55741: contig of
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46372: contig of
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RESULT 1 PFRESAR1 LOCUS

DEFINITION

P.falciparum FC27 surface antigen. x05182 X05182.1 antigen; antigen;

bp Ag46

RESA mRNA

for ring-infected eryrthrocyte

.6-FEB-1998

ACCESSION VERSION

KEYWORDS

tandem repeat

GI:9962

ring-infected erythrocyte surface antigen; surface

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Mol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Data kindly reviewed (10-JUL-1987) by Favaloro For FC27 RESA genomic sequence see X04572; for
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/translation="NSITYNFENINSNVDNGNQSKNISDLSYTDQKEILEKIVSYIVD
ISLYDIENTALNAAEQLLSDNSVDEKTLKKRAQSLKKLSSIMERYAGGKRNDKKSKNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="ring-infected eryrthrocyte surface antigen"
/protein_id="CAA28817.1"
/db_xref="GI:1335718"
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/clone="FC27 Ag46"
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LMSTLKEYLGSSEQMNSITYNFENINSNVDNGNQSKNISDLSYTDQKEILEKIVSYIV
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KKKSRRGWLCCGGGDIETVEPQQEEPVQTVQEQQVNEYGDILPSLRASITNSAINYYD
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NPIVVSQVFGLPFEKPTFTLESPPDIDHTNILGFNEKFMTDVNRYRYSNNYEAIPHIS
EFNPLIVDKVLFDYNEKVDNLGRSGGDIIKKNQTLMDEIMDINKRKYDSLKEKLQKTY
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/db_xref="taxon:5833"
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/gene="RESA"
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RFFFEKRLSMNDLENKSEHLLKFMEQYQKEREAHVSEYLLNILQPCİAGDSKWNVPII
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/protein_id="CAA00077.1"
/db_xref="GI:410748"
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        tggtaatgaaacacgtaagtataaaatgacaagtataagagatgttaagcctacagatgt
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Dorner, F., Scheiflinger, F. and Falkner, F. Gunter.
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                                                                                                                                                                                                                                                                                                                 Unclassified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complete sequence.
AE001373 AE001362
AE001373.1 GI:384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (02-NOV-1998) The Institute for Medical Center Drive, Rockville, MD 20814,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Erratum:[[published 4;282(5395):1827]]
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1 (bases 1 to 12029)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Plasmodium f
/db_xref="taxon:5833"
/chromosome="2"
3709. .5236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       282 (5391), 1126-1132 (1998)
                                                                                                                                                                                                                  /gene="PFB0115w"
6675. .10253
/product="predicted secreted protein"
/protein_id="AAC71813.1"
/protein_id="AAC71813.1"
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TYGDNLQLGASTINTPKTQSQENKDINKETKNTIIKKTNNFPSTLNEKFPHKIOLTNK
ENKEDEQNKENKKDEQNKEDEQNKQNKEDEQNKOKKNIVSNKLSGNNEQQONNSIP
KSIQKFENCVKKQSNQFPRSYPEFFEANFGPIDELMDETDYSSDDLEDDLNYGYRGIE
HDIDETDYYIGSILGYSDFMNKMKYQNTQIDNNKGKKTTNTMEKNKKNDKKHSKKHSKKRK
TKQNYKYKKENQNIENHIPQSKYKQERIEILDDNGKELKSHKNIKEEKGGIEKTDTTN
                                                                                                                                                                                                                                                                                               TRVTEIWKLLLEQMEVKYLIKTDNMNHKWRDFMWESKWALYLENVYKFINDKLNEPHV
SIVEKETFIQKWFINTSHDYNYFLNFVFERWKHKVKSVCEQYEVLLYHICSFLFFLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Join(3709. .4318
                                                                                                                                                                                                                                                                               LFSCIFIYLFLPFLCMFVYLLPFCLFLIINFINKPFM"
                                                                                                                                                                                                                                                                                                                                   EKKYMYQRIIVEREDVIWKQDFKITLNEKSYERLNLPTEKQIPYSTCSEEIEKVHNLT
                                                                                                                                                                                                                                                                                                                                                                   /product="predicted integral membrane protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="pFB0110w"
/note="""
                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                    /note="predicted
                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
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                                                                                                                                                                                                       /gene="PFB0115w"
                                                                                                                                                                                                                                                                                                                                                  translation="MNILVTLFIHTNKIYTIIITYIVLCYLFLCSFYVKKSIKNITR/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          falciparum
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73 of the
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGGTGATCAAGAAAACAAAGAAGAAACAGAAACAGAAAAGCCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGACGACGAAAAAGAAGAACAAGAACAGATGATGAAGAAGATACAGATGATGAAG 7848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tagatgatcaaaatatttcaattgcaggacacactttcattgaccgtccgaactatcaat 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aagaacaggcgagtaaagataaaagcagcaagctaaacctcaaattccgaaagataaat 208
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                                                                                                                                                                                                                                                                                                                                                                                                                               AC021008 201289 bp
Mus musculus chromosome
SEQUENCE SAMPLING.
                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                AC021008
AC021008.3 GI:9887736
                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                                     HTG; HTGS_PHASEO
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ERLRAFYFDKDLTAYYIKKLKDIFKLETEAAKNYYYYVKCQKTESDKKRLYNNLDSIK
LYYESQINKNFISIPKOKIPTAYYIKNLVNDLIFLLPQSNANKAL"
1 1009 c 1093 g 4293 t
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HVRRIKKKMKDDDYDESLKTKNYYPHINTFGQQQYFPYYNPLEQQNYQLHHIIKQQQN
YHPHHIIKQCQNHNPHHILQEQEKHHPQGIPKOPK
OPNIKQGQPHNDDHHIILQEQEKHHPQGIPKNTDVKQDASHIYNNSSEKQIEHYYNKED
OPNIKQGVVKGQEPHYDDMHNITKEHKNFKNTTDVKQDASHIYNNSSEKQIEHYYNKE
PEKQIEHYYNKS PEKQIEHYYNNSPEKQIEHYYNNSPEKQIEHYYNN
NSPEKPARHTNNISLEKQNSHKYNNIQDRHDPVYKYEDMLKRDKDLFTIINNICEL
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11 clone RP23-59C1 r
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                                    Lander, E
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JOURNAL
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Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A.,
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J.,
FitzHugh, W., Forrest, C., Gage, D., Galagan, J.,
Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J.,
Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Howland, J.C., Johnson, R., Jones, C., Liu, G., Locke, K.,
Manders, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K.,
Macdonald, P., Marguls, N., McEvan, P., McGurk, A., McKernan, K.,
Macdonald, P., Marguls, N., McBeus, L., Morrow, J., Naylor, J.,
McDheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J.,
Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K.,
Plerre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,
Don, A. Scance, D. Scance, D. Scance, C., Scance, C., Sance,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (12-JAN-2000) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 24, 2000 this sequence version replaced gi:8980920. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 * However, it should not be assumed that this clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                will be sequenced to completion. In the event that the record is updated, the accession number will
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------ Project Information
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32269: contig of 32369: gap of 33071: contig of

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage BP 191 19106 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
2 (bases 1 to 879)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is from an A. gambiae BAC library provided by F.H. Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J. Direct Submission
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Direct Submission
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Pterygota: Neoptera; Endopterygota; Diptera; Nematocera;
Culicoidea; Culicidae; Anopheles.
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28.58	gb_gss27:*	ss26:	ss25:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No No	Score 74.2 70.6	Query Match 11.9 11.4	th 42 42 93	DB I	ID CNS018GS CNS00880 BE215316
c 5 5 4 7 6 5 4	70.6 69.2 69.2	11.4 11.1 11.1	997 581 942 959	190 191 190	NS01 NS01 NS00
c 8 9 10		11111	1223 639 1101 1135	183 190 190	B12981 CNS017QD CNS0153V CNS033GQ
c 12 c 13	68.4 68.4		870 1101 952	156 190 172	AQ330286 CNS01807
	67.4 67	10.9 10.8	952 1101	172 190	AQ897460 CNS00KHB
c 16	5 5 5 6 6	•	796 1101	190	CNS0118D
	66.2		850	190	CNS009E7
c 19	5 6 6 6		576 963	191	CNS035N7
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	64.4	10.4	1101	190	CNS017QV
	64.2		730	171	AQ879158
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	5 6 4 4	10.3	1043	169	AQ782441
		10.0	726	١	0.000

ALIGNMENTS

RESULT 1
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CNS018GS 942 bp DNA GSS 26-JUL-1999
TION Drosophila melanogaster genome survey sequence T7 end of BAC
BACN13P09 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ION AL109318
N AL109318.1 GI:5629622
DS GSS.

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CNS00880 593 bp DNA GSS 03-JUN-19
Drosophila melanogaster genome survey sequence TET3 end of
BACR16J23 of RPCI-98 library from Drosophila melanogaster (
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant The DNA was prepared from embryos by Alain Bucheton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthrópoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

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/clone="BACN13P09"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Collaboration with the Berkeley Drosophila Genome Project (BBGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org.The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Manmoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                    aagaaccagtatatccaggaccagcaacacctgaacaattaaatagaggtgtaagctttg
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accytccyaactatcaatttacaaatcttaaaycayccaaaaaaggtagtattggtgtact 430
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Determination of this BAC-end sequence was carried out
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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nes 229; Conserv
atattgaaattccagatgctgatattaaagaaccagtatatccaggaccagcaacacctg 283
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100 Jordan Hall, Cl
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE215316 894 bp mRNA EST 25-JUL-2000 HV_CEb0006H11f Hordeum vulgare seedling green leaf EST library HVcDNA0005 (Erysiphe infected & control) Hordeum vulgare cDNA cHV_CEb00006H11f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Development of a genetically and physically anchored for barley genomics Unpublished (2000) Contact: Wing RA Clemson University Genomics Institute
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Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo,Y., Anderson,H., Dale,J., Henry,D., Choi,D.W., Main,D. and
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/lab_host="SOLR"
/note="Vector: lambdaZAP;
/not 41 g 85
                                                                                                                                                                                                                                                                                                    /clone="HV_CEb0006H11f"
/clone_lib="Hordeum vulgare seedling c/
library HVcDNA0005 (Erysiphe infected
/tissue_type="seedling green leaf"
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/cultivar="CI16151 (Mla6)"
/db_xref="taxon:4513"
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/ta; Liliopsida; Poales; Poaceae; Hordeum.
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                                                                                                                                                                                                                                                                                                             - Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
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                                                                                                            /organism="Drosophila m
/plasmid="pbeloBACI1"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN09C07"
/note="end : SP6"
                                                                                                                                                                                                                                ocation/Qualifiers
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Tetraodon nigroviridis
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Eurypterygii; Ctenosquamata; Acanthomorpha; Euacanthomorpha;
Holacanthopterygii; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Tetraodon.
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197M17 of
                                                            Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part o scale clone-end sequencing project of the Tetraodon nigrov genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                     Roest-Crollius,H., Jaillon,O., Dasilva,C., Bound
Bernot,A., Fizames,C., Wincker,P., Brottier,P.,
Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wi
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Roest-Crollius, H.,
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/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                     Bouneau, L.,
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BP 191 91006 EVAL COLL.

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as collaboration with the Berkeley Drosophila Genome Project The BDGP is constructing a physical map of the Drosophila The BDGP is constructing these BACs. For further informations are the second sec
                                                                                                                                                                                               Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                               fly), genomic survey s
AL062806
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                                                                                                                                                                          Drosophila melanogaster genome survey sequence TET3 end of BACR13F18 of RPCI-98 library from Drosophila melanogaster (frui fly), genomic survey semmence
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                                                                                                                GSS
                                                                                          fruit fly.
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/db_xref="taxon:7227"
/clone_libb="RPCI-98"
/clone="BACR35J09"
/note="end : T7"
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                                                                                               gtaaagataaacaattaacattaattacttgtgatgattacaatgaaaagacaggcgttt
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Direct Sub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 collaboration with the Berkeley Drosophila Genome Project (BDY The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was
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/note="end : TET3"
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/db_xref="taxon:7227"
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                             ccgaactatcaatttacaaatcttaaagcagccaaaaaaggtagtattggtgtactttaaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax: 215-898-8780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               University of Pennsylvania
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       jecker@atgenome.bio.upenn.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone="T24D11"
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                                                                                                                                                                                                                                           Matches 185;
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                                   ARAAWWWATGGAGTAAWAAAWATWTAAWRTTTTAAGAAAAAAAAWWGTWGGAWWARAWR
                                                                                                                          gaacaggcgagtaaagataaaaagcagcaagctaaacctcaaattccgaaagataaatcg 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (23-JUL-1999) Genoscope - Centre National de Seq
BP 191 19106 EVKY Cedex - FRANCE (E-mail : seqref@genoscop
- Web : WWW.genoscope.coxs.fr)
Determination of this BAC-end sequence was carried out as
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/clone="BACN37M13"
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/plasmid="pBeloBAC11"
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segref@genoscope.cns.fr
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Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton
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Drosophila melanogaster genome survey sequence
BACN12N03 of DrosBAC library from Drosophila me
fly), genomic survey sequence.

AL104965
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                          Conservative
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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/note="end : T7"
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(phases 1 to 1135)
(bases 1 to 1135)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
                                                                   Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ dat
This sequence is a single read and was generated as
scale clone-end sequencing project of the Tetraodon
genome. For more information, please take a look at
                                                                                                                                                                                                                                                                                                                                                                     Roest-Crollius, H., Jaillon, O., Dasily
Bouneau, L., Billault, A., Quetier, F.,
Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei Eurypterygii; Ctenosquamata; Acanthomorpha; Euacanthomorpha; Holacanthopterygii; Acanthopterygii; Percomorpha;
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208P24 of library G from Tetraodon nigroviridis, genomic survey
                                http://www.genoscope.cns.fr/Tetraodon_
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/organism="Tetraodon nigroviridis"
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AQ330286
AQ330286.1 GI
                                                    Unpublished (1998)
Contact: Wing RA
Clemson University Genomics Institute
                                                                                                 Magnoliophyta; Liliopsida; 1 (bases 1 to 870) Wing, R.A. and Dean, R.A.
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nbxb0046J18r CUGI
         Tel:
Fax:
                                Clemson University
100 Jordan Hall, C
                                                                                                                                               Oryza sativa.
Oryza sativa
                                                                                      A BAC End Sequencing Framework to
                                                                                                                       Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.
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rwing@clemson.edu
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/clone="208P24"
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/clone_Tib="G"
/note="Genoscope sequence ID : COAG208DH12SP1~end
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9%. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening. The second of 
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/clone_lib="CUGI Rice BAC
/tissue_type="Leaf"
/lab_host="E. coli DH10B"
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/strain="Japonica"
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                                                                                              aaaatgaatcactagatgatcaaaatatttcaattgcaggacacactttcattgaccgtc
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                                                                                                                                                                                                                                                                                                                                                           cgaactatcaatttacaaatcttaaagcagccaaaaaaggtagtatggtgtactttaaag
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                                                                      AAAAATAATATAAAAAAAATAATAWAWAAAAAATTAAWTATCAANNCACANTCTTCNCNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre
BP 191 91006 EVRY cedex - FRANCE (E-mail :
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AL108721
AL108721.1 GI:5629025
GSS.
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1 (bases 1 to 1101)
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Drosophila melanogaster genome sur
BACN37F07 of DrosBAC library from
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/clone="BACN37F07"
/note="end : SP6"
a 70 c 85 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Drosophila
/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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atattgaaattccagatgctgatattaaagaaccagtatatccaggaccagcaaccacctg 283
                                                              aagataaaagcagcaagctaaacctcaaattccgaaagataaatcgaaaagtggcaggct 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clones may be purchased from Research Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu Plate: 3134 _row: M column: 12
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HS_3134_A2_G06_T7C CIT Approved Human Genomic Sperm
sapiens genomic clone Plate=3134 Col=12 Row=M, DNA s
AQ897460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             401 Queen Anne Avenue North, Seattle, Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQ897460.1 GI:6353650 GSS.
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University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Mahairas GG, Wallace JC,
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Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota;
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Natl. Acad. Sci. U. S. A. 96
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                                                                                                                                                                                                                                                        /note="Organ: sperm;
E-Coli DH10B"
a 20 c 110 g
                                                                                                                                                                                                                                                                                                                /clone="Plate=3134 Col=12 Row=M"
/clone_lib="CIT Approved Human Go
                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                   /sex="male"
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Pred. No. 4.6e-05;
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Adams,M.D.
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                                                                                                                                                                                                                                         Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammosor in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                      and how to order individual BAC clones, the entire filters for hybridization from the BACPAC Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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                                  /organism="Drosophila n
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR17J10"
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Pred. No. 5.7e-05;
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Search completed: March 14, 2001, 14:04:33 Job time: 41244 sec

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YWIE_CAEEL
NFM_MOUSE
TEGU_HSV60
TOP1_DROME
TEGU_HSV60
TOP1_TEAST
YEAST
PRTE_BACNU
SCP1_MEANU
YEAST
PRTE_BACSU
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Query Match
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Conservative

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Score 97.5; DB Pred. No. 2.6; 32; Mismatches

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34 HDKDKDEKIEQYDKNVKEQASKDKKQQAKPQIPKDKSKVAGYIEIPDADIKEPVYPGPAT

PEQLNRGVSFAEEN---ESLDDQNISIAGHTFIDRPNYQFTNLKAAKKGSMVYFKVGNET HKKDKKEKKEKKDKKEKKD-KKEKKHKKEKKHKKDKKKK-----ENSEVMSLYKTGQHK 180

PK---NATEHGEENLDEEMVSEINNNAQGGLLLSSP-YQYREQGGCGIISSVH-ETSNDT

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Matches 43
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Vitadello M., Vettore S., Lamar E., Chien K.R., Gorza L.;

"Neurofilament M mrNA is expressed in conduction system myocytes of the developing and adult rabbit heart.";

J. Mol. Cell. Cardiol. 28:1833-1844(1996).

-i- FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L. M. AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER.

-i- PTM: THERRE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K.S-P, NFM: THEOGRAPHORYLATED ON A NUMBER OF THE SERINES IN THIS MOTIF. IT IS THOUGHT THAT PHOSPHORYLATION OF NFH RESULTS IN THE FORMATION OF
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01-OCT-1996 (Rel. 34,
01-OCT-2000 (Rel. 40,
NEUROFILAMENT TRIPLET
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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01-0CT-2000 (Rel. 40, Last annotation update)
NEUROFILAMENT TRIPLET M PROTEIN (160 KDA NEUROFILAMENT PROTEIN)
(NEUROFILAMENT MEDIUM POLYPEPTIDE) (NF-M) (FRAGMENT).
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OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H),
LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY A
COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION.
SIMILARITY: BELONGS TO THE INTERNEDIATE FILAMENT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D.
Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., F.
Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K.,
Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.
Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.
Walsh S.V., Whitehead S.;
PEAM; PF00270; DEAD; 1.
PFAM; PF00271; helicase_C; 1.
PROSITE; PS00690; DEAH_ATP_HELICASE; FALSE_NEG.
Hypothetical protein; ATP-binding; RNA-binding;
NP_BIND 107 114 ATP (POTENTIAL).
SITE 209 212 DEAH BOX.
STEE 209 3 AA; 114057 MW; 474DDC99C543171F
                                                                                                                                                                                                                                                                                               Yeast 11:61-78(1995).
-!- SIMILARITY: TO OTHER "DEAH" SUBFAMILY.
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EMBL; X79743; -; NOT_ANNO
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Eukaryota; Fungi; Ascomycota; Saccharomycetes;
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INTERPRO; IPRO01650; -.
INTERPRO; IPRO02464; -.
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Query Match Best Local Matches 4

Similarity

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Score 94.5; Pred. No. 7

DB 1; l; 83;

Length 993; Indels 3

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Gaps

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Conservative

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J. Biol.
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Hart
                                          between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There use by non-profit institutions as long as a modified and this statement is not removed. Us
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"Identification of six phosphorylation sites
tail region of the rat neurofilament protein
J. Biol. Chem. 267:4467-4471(1992).
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Mapolitano E.W., Chin S.S.M., Colman D.R.,
"Complete amino acid sequence and in vitro
the middle molecular weight neurofilament
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01-CT-2000 (Rel. 40, Last annotation update)
NEUROFILAMENT TRIPLET M PROTEIN (160 KDA NEUROFILAMENT PROTEIN)
(NEUROFILAMENT MEDIUM POLYPEPTIDE) (NF-M).
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SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                     PTM: THERE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P, PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THIS MOTIF. IT
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FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M
AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER.
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license@isb-sib.ch).
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              Noback M.A., Terpstra P., Holsappel S., Ve
"A 22 kb DNA sequence in the cspB-glpPFKD
Bacillus subtilis chromosome.";
Microbiology 142:3021-3026(1996).
                                                                                      Bacillus subtilis.
Bacteria; Firmicutes;
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                                       Noback M.A.,
                                               MEDLINE=97124185; PubMed=8969498;
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           or
                                  use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Amphibia; Batrachia; Anura; Mesobatrach:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P50532;
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               XENLA
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TRANSMEM 7 2
                          entities
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                                                                                                                                                                                                                                                                                                    condensation in vitro.";
                                                                                                                                                                                                                                                                                                                                   Hirano T., Mitchison
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
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15-JUL-1998 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                 Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   XCAP-C
                                                                                                                                                                                                                                                                                                                   "A heterodimeric coiled-coil protein required for mitotic chromosome
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                                                                                                                                                SUBCELLULAR LOCATION: NUCLEAR. DURING CHROMOSOME ASSEMBLY IN MITOTIC EXTRACTS, XCAP-C/E WAS RECRUITED TO THE CHROMATIN AND FORMED A DISCRETE INTERNAL STRUCTURE WITHIN ASSEMBLED CHROMOSOMES. DOMAIN: CONSISTS OF TWO PUTATIVE CENTRAL COILED-COIL REGIONS PLANKED BY PUTATIVE GLOBULAR REGIONS AT THE N- AND C-TERMINUS.
                                       European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in ified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ween the Swiss Institute of Bioinformatics
European Bioinformatics Institute. There a
by non-profit institutions as long as i
                                                                                                                                      SIMILARITY: BELONGS TO THE SMC FAMILY.
                                                                                                                                                                                                                                     MITOTIC CHROMOSOMES.
SUBUNIT: ASSOCIATES WITH XCAP-E PROBABLY AS HETERODIMER.
                                                                                                                                                                                                                                                                 FUNCTION: REQUIRED FOR BOTH ASSEMBLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              σ
                                                                                       SWISS-PROT entry is copyright. It is produced through a sen the Swiss Institute of Bioinformatics and the EMBI
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                          requires
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                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus
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         to license@isb-sib.ch).
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21976 MW;
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Pred. No. 1.8;
33; Mismatches
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286C6F96CAA96A43 CRC64;
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                          (See http://www.isb-sib.ch/announce,
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DOMATN
                                                                                                                                            "Identification of the major multiphosphorylation neurofilaments.";
Proc. Natl. Acad. Sci. U.S.A. 85:1998-2002(1988).
                                                                                                                                                                                                                                                            sequence and the relationship of its filament gene family.";
                                                                                                                                                                                                                                                                                                                                                                                     (NEUROFILAMENT MEDIUM POLYPEPTIDE) (NF-M) (NEUROFILAMENT NEFM OR NFM OR NEF3.
                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1988 (Rel. 08, 01-OCT-2000 (Rel. 40, NEUROFILAMENT TRIPLET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEM_HUMAN
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DOMAIN
                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                   EMBO
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"The human mid-size neurofilament subunit: a
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                              Eukaryota;
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Lazzarini R.A.;
                                                                                                                                                                                                             MEDLINE=88158120;
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                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     380 NREKFTQLDLQDVDTREKLKHSKSKVKKLQK--QLQKDKEKVDELKNVPANSQKIIAEET 437
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         PTM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUNCTIONING OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H), THE LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY AND COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION.
                                                                               C. Natl. Acad. Sci. U.S.A. 85:1998-2002(1988).

FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: LEUNCHION.

AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIB

PTM: THERE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P, N

PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THIS MOTIF. IT I

THOUGHT THAT PHOSPHORYLATION OF NEH RESULTS IN THE FORMATION.
                                                           INTERFILAMENT CROSS OF AXONAL CALIBER.
                                                                                                                                                                                                                                                 <u>.</u>
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                                                                                                                                                                                                                                                t gene family.";
6:1617-1626(1987).
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                                                                                                                                                                                                                          OF
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764
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1263
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841
1196
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rini R.A., Lee V.M.-Y.,
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1027
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Primates;
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Last annotation update)
M PROTEIN (160 KDA NEUROFILAMENT PROTEIN)
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                                                                                                                                                                                              Carden M.J., Hollosi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MW;
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18;
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(POTENTIAL).
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                                                                        MAINTENANCE
                                                                                                                                                                       mammalian
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S-P, NFM
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01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
FK506-BINDING NUCLEAR PROTEIN (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE)
(PPIASE) (EC 5.2.1.8) (PROLINE ROTAMASE) (NUCLEOLAR PROLINE ISOMERASE) (FKBP-70).
FPR3 OR NOTAG OF THE PROLINE ROTAMASE)
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                  MEDLINE=95050937; PubMed=7525596;
Benton B.M., Zang J.-H., Thorner J.;
"A novel FK506- and rapamycin-binding
                                                                               SEQUENCE FROM N.A. STRAIN=YNN 214;
                                                                                                                                                             FPR3 OR NPI46 OR YML074C.
Saccharomyces cerevisiae (Baker's
Eukaryota; Fungi; Ascomycota; Sacc
                                                                                                                                                                                                                                                                                                                                                                                         YEAST
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                                                                                                                                          Saccharomycetaceae;
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A27864; A27864.
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0-LINKED (GLCNAC) (BY SIMILARITY).
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J. Biol. Chem. 272:12961-12967(1997).
-i- FUNCTION: PPIASES ACCELERATE THE FOLDING RAPAMYCIN-BINDING PROTEIN. SPECIFICALLY B SEQUENCES. MAY BE INVOLVED IN THE ASSEMBL
                                                                                                                                                                                                                                                       HSSP; P20081; 1YAT. SGD; S0004539; NPI46. INTERPRO; IPRO01179; PFAM; PF00254; FKBP;
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Manning-Krieg U.C., Henriquez R.,
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11; X79379; CAA55924.1; 
3L; X79379; CAB55925.1; 
L; Z46373; CAB86504.1; 
R; S47927; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTM: PHOSPHORYLATED AT TYROSINE AND DEPHOSPHORYLATED PHOSPHOTYROSINE-SPECIFIC PHOSPHOPROTEIN PHOSPHATASE I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION PEPTIDE BONDS IN OLIGOPEPTIDES. ENZYME REGULATION: IMPLIBITED BY BOTH FK506 A SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLUS.
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PS00454; FKBP_PPIASE_2; 1.
PS50059; FKBP_PPIASE_3; 1.
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(OCT-1994) to
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ASP/GLU-RICH (HIGHLY ACIDIC)
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, FPR3.";
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PMSR_HELPY
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CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                    Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A. Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S., Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.H., McKenney K., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M. Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M., Venter J.C.;
                                                                                  TIGR;
                                                                                                                                                                                                                                                            Nature 388:539-547(1997).

Nature 388:539-547(1997).

-!- FUNCTION: COULD HAVE AN IMPORTANT FUNCTION AS A REPAIR ENZYME PROTEINS THAT HAVE BEEN INACTIVATED BY OXIDATION. CATALYZES THE REVERSIBLE OXIDATION-REDUCTION OF METHIONINE IN PROTEINS TO METHIONINE (BY SIMILARITY).

-!- SIMILARITY: TO OTHER BACTERIAL AND EUKARYOTIC PEPTIDE METHIONI
                       PFAM; PF01641; DUF25; 1. PFAM; PF01625; PMSR; 1.
                                                                                                                            or send an
                                                                                                                                                           modified
                                                                                                                                                                                          the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=26695 / ATCC 700392;
MEDLINE=97394467; PubMed=92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
PEPTIDE METHIONINE SULFOXIDE REDUCTASE (PEPTIDE
                                                   INTERPRO; IPR002579; -.
                                                                                                                                             entities requires
                                                                                                                                                                                                                        This
                                                                                                                                                                                                                                                                                                                                                         pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Helicobacter pylori (Campylobacter pylori).
Bacteria: Proteobacteria; epsilon subdivisi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MSRA OR HP0224.
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                                                                                                                                                                                                                                                                                                                                                                       "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Helicobacter
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                                                                                                                                                                                      European Bioinformatics Institute.
                                                                                                                                                                                                                                                    SULFOXIDE REDUCTASES
                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNDGEEEQEEEEEEQKEEVKPEPKKSKKEKKRKHEEKEEEKKAK--KVKKVEFKKDLEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LKNGKVFDKNTSGKPFAFKLGRGEVIKGWDIGVAGMSVGGERRIII 380
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                                                                                AE000542; AAD07291.1;
HP0224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity
35; Conser
                                                                                                             non-profit institutions usage by and the statement is not removed. Usage by and the statement is not removed. Usage by and the requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       411 AA;
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> EEE (IN REF. 1).
> F (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                subdivision;
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No. 5.
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Q23525;
                                                                                                                                                                                                            Hypothetical SEQUENCE 4
                                                                                                                                                                                                                                              EMBL; U29380; AAA68745.1; -.
                                                                                                                                                                                                                                                                               use by non-profit institutions a modified and this statement is not entitles requires a license agreeme
                                                                                                                                                                                                                                                                                                                       the
                                                                                                                                                                                                                                                                                                                                             This
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhabditidae; [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans
Eukaryota; Metazoa; Ner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL
                                                                                                                                                                                                                                    WORMPEP;
                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                  between
                                                                                                                                                                                                                                                                                                                                                                                              Submitted
                                                                                                                                                                                                                                                                                                                                                                                                         Hallsworth K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2K546.14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1999
15-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 FAKPHIDNYLHD--KDKDEKIEQYDKNVKEQASKDKKQQAKPQIPKDKSKVAGYIEIP--
                                                                                                                                                                                                                                                                                                                                                                   mitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR (BY SIMILARITY).
SIMILARITY: BELONGS TO THE SURF6 FAMILY.
                                                                                                                                                                                                                                                                                                                     European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
 KLKEMKVERKGKGPAKVTSAMAEKMAEEKRLKRRESKLKLKQRRA---
                                                                                                                    KPHIDNYLHDKDKDEKIEQYD----KNVKEQASKDKKQQAKPQIPKDKSKVAGYIEIPD
                         QFTNLKAAKKG-----
                                              SDSTDEEEETPSKPNKTVAQSTLKSNGKIDKEIQKLEDDE--DNESPEIRRQIALLRLQK
                                                                                             KADSDSEEDDSSDDEEKEETDEPVAKKQKKEESSDDDEDSEDGEEPEGNN----GAVEAED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YLKKHPSGYCHIDLKKADEVIVDDDKYTKPSDEVLKKKLTKLQYEVTQNK---HTEKPFE
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48; Conser
                                                                                                                                                          Similarity
                                                                                                                                                                                                                                   ZK546.14; CE02914
                                                                                                                                                                                                           al protein; Nuclear protein.
472 AA; 54261 MW; 56EA30387545D3DD
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54.3
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38,
38,
KDA
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                                                                                                                                                                                                                                                                                                      institutions as long as its content
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21.8%;
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25.1%;
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Last annotation update)
PROTEIN ZK546.14 IN CHROMOSOME
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                     -SMVYFKVGNETRKYKMTSIRDVKPTDVGVLDEQKGKD-----
                                                                                                                                               40;
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Pred. No. 5.4;
20; Mismatches
                                                                                                                                                         Score
Pred.
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                                                                     QLNRGVSFAEENESLDDQNISIAGHTFIDRPNY
                                                                                                                                               Mismatches
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7.6;
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Qγ

177

KQLTLITCDDYNEKTGVWEKRK

198

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RESULT 11
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                                                                                                                                                                                                                                                                   between the brain or restrictions as long as its content is in no way use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NFM_MOUSE STANDARD; PRT; 848 AA.
P08553; Q61961;
01-AUG-1988 (Rel. 08, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
RUUROFILAMENT TRIPLET M PROTEIN (160 KDA NEUROFILAMENT PROTEIN)
(NEUROFILAMENT MEDIUM POLYPEPTIDE) (NF-M).
                                                                     DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                             EMBL;
             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 322-540 FROM N.A. MEDLINE=87158637; PubMed=3103856; Julien J.-P., Meyer D., Flavell D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                Phosphorylation; INIT_MET 0
                                                                                                                                                                                                                     MGD;
                                                                                                                                                                                                                                                                                                                                                                                  This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Julien J.-P., Meyer D., Flavell D., Hursu
"Cloning and developmental expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Levy E., Liem R.K.H., D'Eustachio P., Cowan N.J.; "Structure and evolutionary origin of the gene encoding the middle-molecular-mass neurofilament protein.";
                                           DOMAIN
                                                        DOMAIN
                                                                                                                 DOMAIN
                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=87246694;
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                                                                                                                                                            Intermediate
                                                                                                                                                                                                        INTERPRO;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M, AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER. PTM: THERE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P, NEW IS PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THIS MOTIF IT IS THOUGHT THAT PHOSPHORYLATION OF NFH RESULTS IN THE FORMATION OF INTERFILAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANCE OF ACCURATE CALLERS.
                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                         PTM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUNCTIONING OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H), THE LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY AND COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION.
                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a sen the Swiss Institute of Bioinformatics and the EMBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   family
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                                                                                                                                                                                                                     MGI:97314; NFM.
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                                                                                                                                                                                                                                  S00030; S00030
                                                                                                                                                                                                                                               X05640; CAA29127.1; -. M20481; AAA39815.1; -.
                                                                                                                                                                                         PF00038;
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                                                                                                                                                                           PS00226; IF; 1.
                                                                                                                                                                                                      IPR001664; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     387:243-250(1986).
                                                                                                                                                          filament; Heptad
                                                                                                                                                                                         filament; 1.
                                                                                                                                              Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=3036526;
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147
246
263
285
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TAIL.
COIL 1A.
LINKER 1.
COIL 1B.
LINKER 12.
COIL 2A.
LINKER 2.
                                                                                                 ROD
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Sciurognathi; Muridae;
                                                                                                                                                          repeat pattern; Coiled coil; Neurone;
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; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neurofilament
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                                                                                                                                                                                                                                                                                                                                                                               collaboration
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В γQ

1840

MTFAMYIDIIEKTYLLCMRHLENVLHDKDFQSVLRARTFDIDYILKQSWTKNIVEHSLFS 1899

9

MTIAGVVLILVAAYLFAKPHIDNYLHDKDKDEKI----

Query Match Best Local S Matches 48

Similarity 48; Conser

Conservative

21

. 68;

Score 87; DB Pred. No. 67; 23; Mismatches

DВ 67;

Length 2077;

79;

72;

Gaps

----EQYDKNVKEQA---

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RESULT 12
TEGU_HSV6U
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Best Local S
Matches 41
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01-OCT-1996
01-OCT-1996
01-OCT-1996
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CARBOHYD
CARBOHYD
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                           Gompels U.A., Nicholas J., Lawrence G., Jones M., Th
Martin M.E., Efstathiou S., Craxton M., Macaulay H.A
"The DNA sequence of human herpesvirus-6: structure,
 EMBL; X83413; CAA58411.1; SEQUENCE 2077 AA; 2399
                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                          use by non-profit institutions as long modified and this statement is not removed.
                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre European Bioinformatics Institute. There are no restitute the European Bioinformatics Institute.
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=95266321; PubMed=7747482;
                                                                                                                                                                                                                                                                                                        U31 OR HHRF1
                                                                                                                                                         Virology 209:29-51(1995).
                                                                                                                                                                                                                                                                               Herpes simplex virus (type 6 / Viruses; dsDNA viruses, no RNA
                                                                                                                                                                                 and genome evolution.
                                                                                                                                                                                                                                                                     Betaherpesvirinae; Roseolovirus.
                                                                                                                                                                                                                                                                                                                     LARGE TEGUMENT
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                                                                                                                         SIMILARITY: BELONGS TO FAMILY 1
EHV-1 24, EBV BPLF1, HVS-1 64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KPHIDNYLHDKDKDEKIEQYDKNVKEQASKDKKQQAKPQIPK---DKSKVAGYIEIPDAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKD 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIAINGEVEGKEEEEQETQ----EKGS-----GREEEKGVVTNGLDVSPA-----EEKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NISIAGHTFIDRPNYQFTNLKAAKKGSMYYFKYGNETRKYKMTSIRDYKPTDYGYLDEQK
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47
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432
539
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47 0
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432 S
540 95910 MW;
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239946 MW;
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                                                                                                                                                                                                                                                                                                                                          sequence
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S -> F (IN REF.
QA -> RR (IN REF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 88; DB
Pred. No. 19;
29; Mismatches
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O-LINKED
                                                                                                                                                                                                                                                                               / strain
\ stage;
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 C1CA4BDC26650511 CRC64;
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                                                                                                                                 THAT, VZV
                                                                                                                                                                                                                                                                                                                                          update)
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Herpesviridae;
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                                                      ormatics and the EMBL outstati
There are no restrictions on
ong as its content is in no
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                                                                                                                                GROUPS TOGETHER HSV-1 UL36, 22, AND HCMV UL48.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 848
                                                                                                                                                                                                       H.A.;
                                                                                                                                                                                                                     Thomson B.J.,
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SIMILARITY).
                                                                                                                                                                                           coding
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                                                                                                                                                                                             content,
                                                                                                         collaboration
                                                                                                 outstation
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                                                           in no way commercial
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RESULT 13
TOP1_DROME
ID TOP1_DROME
ID TOP1_DROME
ID 01-APR
DT 01-APR
DT 01-APR
DT 01-OCT
DE DWA'S
GN TOP1.
OS DROSOP
OC ENLKARY
OC ENLKARY
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RN SEQUEN
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J. Cell Biol. 134:923-934(1996).

J. Cell Biol. 134:923-934(1996).

FUNCTION: THE REACTION CATALYZED BY TOPOISOMERASES LEADS TO THE CONVERSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER.

CONVERSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER.

I. CATALYTIC ACTIVITY: ATP-INDEPENDENT BREAKAGE OF SINGLE-STRANDED DNA, FOLLOWED BY PASSAGE AND REJOINING.

II CAN RELAX BOTH NESCRILLS EUKARYOTIC TOPOISOMERASE I AND II CAN RELAX BOTH NESCRILLANEOUS: EUKARYOTIC TOPOISOMERASE TRANSIENTLY BREAKS A DNA BACKBONE BOND, IT SIMULTANEOUSLY FORMS A PROTEIN-DNA LINK, IN WHICH A TYROSYL OXYGEN IN THE ENZYME IS JOINED TO A DNA PHOSPHORUS AT ONE END OF THE ENZYME-SEVERED DNA STRAND.

II SIMULTANEOUSLY FORMS A PROTEIN-DNA PHOSPHORUS AT ONE END OF THE ENZYME-SEVERED DNA STRAND.
                                                  modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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01-APR-1993 (Rel.
01-OCT-2000 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2011
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                                                                                                                                                                                                                                                                    EMBL; M74557; AAA28951.1; EMBL; U80064; AAC24158.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96354910; PubMed=8769417;
Zhang C.X., Lee M.P., Chen A.D., Brown S.D., Hsieh T.-S.;
"Isolation and characterization of a Drosophila gene essential
early embryonic development and formation of cortical cleavage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                        FLYBASE; FBgn0004924; Top1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-OREGON-R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93117086; PubMed=1335568;
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                                                              Hypothetical protein; ATP-binding. NP_BIND 8 15 ATP (NON TER 195 195 SEQUENCE 195 AA; 21135 MW; D7F
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                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                              Unpublished observations
                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=ATCC 13869;
                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation updat
HYPOTHETICAL PROTEIN IN PTSG 3'REGION (FRAG
                                                                                                                PFAM; PF01121; UPF0038; 1.
PROSITE; PS01294; UPF0038;
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 1 Similarity 28.4
44; Conservative
                                                                                                                                         IPR001977;
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                                                                                                                                                                 NOT_ANNOTATED_CDS.
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198 SER-RICH.
930 DNA CLEAVAGE (BY SIMILARITY).
111688 MW; 3764B8BDEEFA3OCD CRC64;
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22.7%;
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 Score 84.5; D
Pred. No. 5.7;
21; Mismatches
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38;
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65 IPKDKSKVAGYIE-----IPDAD--IKEPVYPG-PATPEQLNR-GVSFAEENESLDDQNI 115

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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
[1]
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p54397;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
39 KDA FK506-BINDING NUCLEAR PROTEIN (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (PPIASE) (EC 5.2.1.8).
FK506-BP1 OR FKBP39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunosuppressive drug FK506.";
Gene 156:247-251(1995).
-!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
MAY FUNCTION IN A SIGNAL TRANSDUCTION CASCADE DURING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95278752; PubMed=7538962;
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                                                                                                                                                                                                                                                                                                         PROSITE; PS00453; FKBP_PPIASE_1; FALSE_NEG
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TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED, HIGHEST LEVELS
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                                                                                                                                                                                                                                                                                                                                      PF00254; FKBP;
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119
186
                                                                                                    AA;
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183
247
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7.98;
27.68;
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                                                                                                    MW;
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ASP/GLU-RICH (HIGHI
ASP/GLU-RICH (HIGHI
ASP/GLU-RICH (BASIC).
LYS-RICH (BASIC).
PPIASE, FKBP-TYPE.
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Score 84.5;
Pred. No. 12;
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                      DVKPTDVGVLDEQKGKDKQLTLITC
                                                  DQVVGKGEEAKQGKRVSV---YYIGRLQSNNKTFDSLLKGKPFKFALGGG---
                                                                         EE----NESLDDQNISIAGHTFIDRPNYQFTNLKAAKKGSMVYFKVGNETRKYKMTSIR 159
                                                                                                  KSGKEQNGVAKKEEAKQQ-QKKKEKPEAKKEQPKA--KEPAKQQPASKDPRTITGGVKIV 256
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326
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Search completed: March 2, 2001, 10:24:33 Job time: 120 sec

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Minimum
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Copyright (c) 1993 - 2000 Compugen Ltd
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_66:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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hypothetical protein C32E12.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te: C;Accession: T25593 R;Wilcox, L.

15-Oct-1999 #text_change 15-Oct-1999

submitted to the EMBL Data Library, November 1996 A;Description: The sequence of C. elegans cosmid (A;Reference number: Z20055 A;Accession: T25593

A;Status: preliminary; translated from GB/EMBL/DDBJ

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
84.5	84.5	84.5	85	85	85	85	85	86.5	87	87	87	87	87	87.5	88
7.9	7.9	7.9	7.9	7.9	7.9	7.9	7.9	8.0	8.1	8.1	8.1	8.1	8.1	8.1	8.2
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gene NS-1 protein	FK506-binding 39k	probable integral	DNA topoisomerase	hypothetical prote		hypothetical prote	conserved hypothet	hypothetical prote	tegument protein -	liver stage antige	hypothetical prote	outer membrane pro	hypothetical prote	probable hydrolyti	hypothetical prote

ALIGNMENTS

R:Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, submitted to the EMBL Data Library, June 1999
A; Reference number: Z21612
A; Accession: T36719
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molocule trace. Nan probable integral membrane protein - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 C;Accession: T36719 C;Accession: T36719 Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajano 밁 δÃ Db Qγ 밁 QY DЬ A;Molecule type: DNA A;Res.dues: 1-352 <MUR> A;Cross-references: EMBL:AL079308; PIDN:CAB45217.1; GSPDB:GN00070; SCOEDB:SCH69.20c A;Experimental source: strain A3(2) RESULT T36719 A; Gene: SCOEDB: SCH69.20c Query Match Best Local S Matches 47 313 RYITLTTCTPEFTSKYRMIVWGK 335 177 KQLTLITC-DDYNEKTG--VWEK 196 124 148 GVLMLLFVTYQLWWTNVRAH------AQANQAASNLQDDWANGKRS------PGSFEPG 194 255 HGEPFRYIN--KLEPGDPIVVETQDKYFVYKMASILPVTSPSNVSVLDPVPKQSGFKGPG 312 195 QGFALLHIPKLDVVVPIAEGISSKKVLDRGMVGHYAEDGLKTAMPDAKAGNFGLAGHRNT 254 73 AGY--IEIPDADIKEPVYPGPATPEQLNRGV--SFAEE--NESLDDQ---NISIAGHTFI 123 13 GVVLILVAAYLFAKPHIDNYLHDKDKDEKIEQYDKNVKEQASKDKKQQAKPQIPKDKSKV 72 Local Similarity 23.1 Local Similarity 23.1 Local Similarity 23.1 DRPNYQFTNLKAAKKGSMVYFKVGNETRKYKMTSIRDV-KPTDVGVLDEQ------KGKD 176 9.7%; 40; Score 104; DB 2; Pred. No. 0.61; 0; Mismatches 82 Parkhill, J.; Barrell, B.G.; Rajandream, M.A 1999 82; Length 352; Indels 34; Gaps 11;

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RESULT
A54514
glutamic acid-rich protein precursor
N;Alternate names: GARP
C;Species: Plasmodium falciparum
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A;Cross-references: EMBL:AL117203; NID:e1549827;
A;Experimental source: clone Y48C3A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein Y48C3A.a - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct.1999 #sequence_revision 29-Oct.1999 #te: C;Accession: T31583
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A; Introns: 5/2;
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A; Residues: 1-552 <WIL>
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A:Tn+rons: 89/2; 506/3;
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A; Residues: 1-1089 <
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, A; Reference number: Z21046
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                                                                                                               KDPVVPEPMDFGKIQLPERRTREYLSRKAKLAEKN 1036
                                                                                                                                                                            PSPAHIQQLPSNLAPKLSQTKAQEAKNSNDTNIQNLSRDINVPRDTNKHQTEVEDCYAEY 1001
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Pred. No. 3.
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Qy
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C:Superfamily: unassigned ribonucleoprotein repeat-containing
F:3-84/Domain: ribonucleoprotein repeat homology <RRM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, July 1995 A; Description: The sequence of S. cerevisiae
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δõ
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                                                                                                                                                                            В
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                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-887 < NEL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N;Alternate names: hypothetical protein PRR112c - yeast (Saccharomyces N;Alternate names: hypothetical protein P8283.19 C;Species: Saccharomyces cerevisiae C;Date: 13-Jan-1996 *sequence_revision 01-Mar-1996 *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DЬ
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C; Superfamily: histone
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A; Residues: 1-678 <TRI>
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A; Accession: A54514
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                                                                  ----DRPNYQFTNLKAAKKGSMVYFKVGNETR---
 EQKGKDKQ 178
                                                                                                                                    YIEIPDADIKEPYYPGPATPEQLNRGVSFAEENESL--DDQNISIAGHTFI------
                                                                                                                                                                        FADPRVPQPMKEKRREALKRFREKEEKLLQEENRKKKKVDENKHSNIDDEIRKNKQL---
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42; Conserv
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18.6%;
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6.7;
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A;Cross-references: EMBL:X79743
A;Cross-references: EMBL:X79743
A;Note: the nucleotide sequence was submitted to the EM A;Note: the nucleotide sequence was submitted to the EM C:Genetics:
A;Map position: 9R
C;Superfamily: unassigned DEAD/H box helicases; DEAD/H
C;Keywords: ATP: P-loop
F;107-610/Domain: DEAD/H box helicase homology <DEAD>
F;107-114/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                           probable RNA helicase YIR002c - yeast (Saccharomyces K;Alternate names: hypothetical protein YIB2c C;Species: Saccharomyces cerevisiae C;Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #t C;Accession: S48436; S50885 R;Badcock, K.; Churcher, C. submitted to the EMBL Data Library, August 1994 A;Reference number: S48432 A;Reference number: S48432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: mRNA
A;Residus: 1-644 <VITY
A;Cross-references: EMBL:247378; NID:9854352; PIDN:CAA87454.1; PID:9854353
C;Superfamily: cytoskeletal keratin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neurofilament protein M - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_char
C;Accession: S55395
R;Vitadello, M.; Vettore, S.; Lamar, E.; Chien, K.R.; Gorza,
Submitted to the EMBL Data Library, January 1995
A;Bescription: Neurofilament mRNA and protein are expressed i
A;Reference number: S55395
A;Accession: S55395
                                                                                                                                                                                                          A;Cross-references: GB:Z47047; EMBL:Z38062; NID:g603997; PID:g763347; MIDS:YIR002c R;Voss, H.; Tamamos, J.; Teodoru, C.; Valencia, A.; Sensen, C.; Wiemann, S.; Schwag Yeast 11, 61-78, 1995
A;Title: Nucleotide sequence and analysis of the centromeric region of yeast chrome A;Reference number: S50795; MUID:95282515
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S48436
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A; Residues: 1-993 <BAD>
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                                                                                                                                                                            A; Status: nucleic
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Best Local S
Matches 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --DADIKEPVYPGPATPEQLNRGVSFAEENESLDD-----QNISIAGHTFIDRPNYQF 130
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   RESULT 9
$73663
hypothetical protein P02_orf253 - My
C;Species: Mycoplasma pneumoniae
A;Variety: ATCC 29342
C;Date: 27-Feb-1997 #sequence_revisi
C;Accession: $73663
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A;Gene: ATSP:T15N24.80
A;Map position: 4
A;Introns: 345/3; 357/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:AL078465; GSPDB:GN00062; ATSP:T15N24.80 A;Experimental source: cultivar Columbia; BAC clone T15N24 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-763 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;205-210/Region: nucleotide-binding F;209-212/Region: DEAD/H motif
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Best Local
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Best Local
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                                                                                                                    183 TCDDYNEKTGVWEKRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 23.0 Local Similarity 23.0
                                                                                    NGDENKQVENVEGKEK
                                                                                                                                                                                                                         DEDADGKK-----EQTDDGVSVEDTVMKENVESKDN--
                                                                                                                                                                                                                                                       IPDADIKEPVYPGPATPEQLNRGVS-----FAEENESLDDQNISIAGHTFIDRPNYQFTN 132
                                                                                                                                                                                                                                                                                                                          AKPHIDNYLHD----KDKDEKIEQYDKNVKEQASKD----KKQQAKPQIPKDKSKVAGYIE 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NEKTGVWEKRKIFVAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GMGKTFIASTVMLNYFRWTKKAKIIFTAPTRPLVAQQIKACLGITGIPSDQTAILLDKSR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GQKTVYEEIQRDVSFGPTHHELDYDALSFYVYPTNYEVRDYQYTIVHKSLFQNTLCAIPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DDYFSDFEDDELDKLYEKAINKSVKETITRRA----VPVQK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNYLHDKDKDEKIEQYDKNYKEQASKDKKQQAKPQIPKDKSKVAGYIEIPDADIKEPVYP
                                                                                                                                                        EKETKETDITEADHKKAGKEDIQHEADKANGTKDGNTGDIKEEGTLVDEDKGTDMDEKVE
                                                                                                                                                                                      LKAAKKGSMV---YFKVGNETRKYKMTSIRDVKPTDVG-----VLDEQKGKDKQLTLI 182
                                                                                                                                                                                                                                                                                          AEP--DNMEIDAQIKKDDEKAETEDKESEVKKNEDNAETQKMEEKVEVTKDEGQAEATNM 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GPATP-EQLNRGVSFAEENESLDDQNISIAGH-TFIDRPNYQFTNL-KAAKKGSMYYFKV 146
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                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                               384/3; 404/3; 441/3; 472/3; 500/3; 667/1; 697/3; 708/1
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23.0%;
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                                                                                                                                                                                                                                                                                                                                                        27; Mismatches
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Pred. No. 12;
31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                            Score 93.5;
Pred. No. 10;
Mycoplasma
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   ATCC
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#sequence_revision

25-Apr-1997 #text_change 07-Dec-1999

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R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Nucleic Acids Res. 24, 4420-4449, 1996
A;Title: Complete sequence analysis of the genome of the A;Reference number: S7327; MUID:97105885
A;Accession: S73663
A;Status: preliminary; nucleic acid sequence not shown;
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T25994
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C;Superfamily: hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:AE000032; GB:U00089; A;Note: the nucleotide sequence was submitted C;Genetics:
                                                                                                                                                                                                                                                                                                                      A; Map position:
A; Introns: 41/1
                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:U88172; PIDN:AAB42258.1; GSPDB:GN00022; CESP:ZK354.3 A;Experimental source: strain Bristol N2; clone ZK354
                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-312 < JOH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Description: The sequence
A; Reference number: Z20120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, February 1997 A; Description: The sequence of C. elegans cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
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A; Residues: 1-253 <HIM>
                                                                                                                                                                                                                                                                                                                                                       A; Gene: CESP: ZK354.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: T25994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Johnson, D.; Wamsley, P.; Bradshaw,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein ZK354.3 - Caenorhabditis elegans
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mes 48; Conserv
                                                                                                                                                                                  30 DNYLHDK---DKDEKIEQYDKNVKEQASKDKKQQ--AKPQIPKDKSKVAGYIEIPDADIK 84
                                                                                                                                                                                                                           Local Similarity es 37; Conser
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                                                                           DALVENPIVTEMSDRD----EKKEEKKD------
---EEKKEEKKEEKKEEKEE--KKDDKKEDDKEKSATKSEDKKSDEKKTEEKK 299
                                                                                                                                                   DEKMDDKKPGEKEEKKEEFKKEMKKEEKKEEEKKEEPKKNDAPKKEGETKGEVK-----K
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                                    KVGNETRKYKMTSIRDVKPTDVGVLDEQKGKDKQLTLITCDDYNEKTGVWEKRK 198
                                                                                                            EPVYPGPATPEQLNRGVSFAEENESLDDQNISIAGHTFIDRPNYQFTNLKAAKKGSMYYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FKDLSIEAKLSYNFNWFGDYSLGGFT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LFLLCGTVL---SAYTGIQADLRNLIKETTKKDIDVYKAIKTTEGKKNIITSLKKSYEVN
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21.3%;
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22.6%;
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                                                                                                                                                                                                                           35;
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                                                                                                                                                                                                                         Score 91.5; D
Pred. No. 5;
B5; Mismatches
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Pred. No.
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                                                                                                                                                                                                                                                              DB 2;
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nber 1996
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A; Molecule type: mRNA
A; Residues: 1-17,19-21, 'p',23-204,'L',206-500,'E',501-845 <KEL>
A; Cross-references: EMBL: Z12152; NID: 956751; PIDN: CAA78136.1; PI
R; Xu, Z.S.; Liu, W.S.; Willard, M.B.
J. Biol. Chem. 267, 4467-4471, 1992
A; Title: Identification of 4471, 1992
A; Title: Tentification of 4471, Phosphorylation sites in the COOH
A; Reference number: A42393; MUID: 92165797
A; Accession: A42393
                                                                                                                                                                                                                                                                                                              R;Kelly, B.M.; Gillespie, C.S.; Sherman, D.L.; Brophy, J. Cell Biol. 118, 397-410, 1992
A;Title: Schwann cells of the myelin-forming phenotype A;Reference number: S25712; MUID:92332596
A;Accession: S25712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_cha
C;Accession: A45669; S25712; A42393
R;Napolitano, E.W.; Chin, S.S.M.; Colman, D.R.; Liem, R.K.H.
J. Neurosci. 7, 2590-2599, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db
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A; Molecule type: nucleic acid
A; Residues: 411-500, 'E', 501-843, 'D'
                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:M18628; NID:g205687; PIDN:AAA41696.1; R;Keily, B.M.; Gillespie, C.S.; Sherman, D.L.; Brophy, P.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-845 <NAP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Complete amino acid sequence and A;Reference number: A45669; MUID:87282618 A;Accession: A45669
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A;Title: Complete sequence analysis of the genome of the bacterium A;Reference number: S73327; MUID:97105885
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                                                   A; Status: preliminary; not compared with conceptual translation
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submitted to the Protein Sequence Database, January 2000
A; Reference number: Z23036
A; Accession: T46486
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-1288 <AAA>
A; Cross-references: EMBL.AL136877
A; Experimental source: adult testis; clone DKFZp434F205
C; Genetics:
A; Note: DKFZp434F205.1
C; Superfamily: chromosome segregation protein SMC1
    hypothetical protein yhcs - Bacillus subtilis C;Species: Bacillus subtilis C;Species: Bacillus subtilis C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999 C;Accession: G69823 R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chromosomal protein CAPC homolog DKFZp434F205.1 [similarity] - human c;Specles: Homo saplens (man) C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 02-Jun-2000 C;Accession: T46486 R;Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Weil, B.; Wiemann, S.
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20.1%;
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C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997

A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galiech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiquchi, J.; Sekowska, A.; Sakeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida A; Authors: Yoshikawa, H.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A; Terpstra, P.; Schroeter, R.; Yoshida A; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili A. Reference number: A69580; MUID:98044033
                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-1290 <HIR>
A;Cross-references: GB:Ul3673; NID:g563811; PIDN:AAA64679.1; PID:g563812
C;Superfamily: chromosome segregation protein SMC1
C;Keywords: chromosomal protein; DNA condensation; heterodimer
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C;Species: Xenopus laevis (African clawed frog)
C;Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 02-Jun-2000
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A; Residues: 1-198 < KUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: A55094
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A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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320 YIHDLQKRSRDKEAQKEKIQEDTKDISEKSNTLLETMKEKNKALKDVEKQLNKITKFIEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 TLQHEK---EELILTTCYPFS-YVGNAPKRYIIYGKRV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168 VLDEQKGKDKQLTLITCDDYNEKTGVWEKRKIFVATEV
                                                            32 YLHD-----KDKD---EKIEQYDKNVKEQA-----SKDKKQQAKPQIPKDKSKVAGYIE- 77
                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 GTKNSTDQAKNKASFKPETGQASGILEIPKINAELPIVEG-TDADDLEKGVGHYKDSYYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55 --KDKKQQA--KPQIPKDKSKVAGYIEIPDADIKEPVYPGPATPEQLNRGVSFAEENESL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKKVIPLFIIAAGLVIAGYGGFKLI------DTNTKTEQTLKEAKLAAKKPQEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DENGQIVLSGHR-----DTVFRRTGELEKGDQLRLLLSYGEFTYEIVKTKIVDKDDTSII 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DDQ-NISTAGHTFIDRPNYQFTNLKAAKKGSM--VYFKVGNETRKYKMTSIRDVKPTDVG 167
                                                                                                                                       Similarity 36; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                    Score 91; DB
Pred. No. 31;
13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 91; DB 2; Length 198; Pred. No. 3.2;
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 SPTREMBL_15:*

1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb:
6: sp_mammal:*
7: sp_mhc:*
8: sp_organel1:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:
12: sp_virus:*
13: sp_vertebrs:
13: sp_vertebrs:
14: sp_unclass:
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Gapop 10.0 , Gapext 0.5
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1076
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                                                                                                                                                                      sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*
                               sp_plant:*
sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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8.5	8.5	8.6	8.6	8.7	8.7	9.0	9.0	9.1	9.1	9.4	9.5	9.7	9.9	11.7	12.4	17.0	17.1	100.0	Query Match
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	Q9rpe0 mycoplasma	Q9xv10 caenorhabdi		O96154 plasmodium		P72538 streptococc			Q9ufr9 homo sapien		044741 caenorhabdi	Q65023 aleutian mi	Q9zmk8 helicobacte	O85224 helicobacte	Q39448 cicer ariet	Q9z6u5 chlamydia p	09rb58 chlamydia p	O96127 plasmodium	Q9ueq7 homo sapien	Q9k5s8 bacillus ha	P93826 arabidopsis	Q9ntj3 homo sapien	095 7 52 homo sapien	Q9unt9 homo sapien	Q63370 rattus norv

ALIGNMENTS

Qy	рр	Db	Qy	Db	Qy	M B C	SQ	DR E	<u> </u>	RT	RA	RX	RC	RP.	0 0	2 8	3 8	SO	GN	DE	DJ CI) t	P A	ID	Q9S446	RESULT	
181 LITCDDYNEKTGVWEKRKIFVATEVK 206	121 TFIDRPNYGFTNLKAAKKGSMYYFKVGNETRKYKMTSIRDVKPTDVGVLDEQKGKDKQLT 180 	61 AKPQIPKDKSKVAGYIEIPDADIKEPVYPGPATPEQLNRGVSFAEENESLDDQNISIAGH 120	61 AKPQIPKDKSKVAGYIEIPDADIKEPVYPGPATPEQLNRGVSFAEENESLDDQNISIAGH 120	1 MKKWTNRLMTIAGVVLILVAAYLFAKPHIDNYLHDKDKDEKIEQYDKNVKEQASKDKKQQ 60	1 MKKWTURLMTIAGVVLILVAAYLFAKPHIDNYLHDKDKDEKIEQVDKNVKEQASKDKKQQ 60	Ouery Match 100.0%; Score 1076; DB 2; Length 206; Best Local Similarity 100.0%; Pred. No. 4.3e-76; Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps	SEQUENCE 206 AA; 23541 MW; DC3E65C51E145C7B CRC64;	EMBL: AF162687: AAD48437.1:	proteins to the cell Wall."; Science 285:760-763/1999)	"Staphylococcus aureus sortase, an enzyme that anchors surface	Mazmanian S.K., Liu G., Ton-That H., Schneewind O.;	MEDLINE=99357874; PubMed=10427003;		SEQUENCE FROM N.A.	[1]	pactitus/scaphytococcus group; scaphytococcus. NCRT TayTD=1980:	Bacteria; Firmicutes; Bacillus/Clostridium group;	Staphylococcus aureus.	SRTA.		01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)	(III DEDUCE 1. 13, CIEC	(TrEMBIre) 13	Q9S446 PRELIMINARY; PRT; 206 AA.	46	LT 1	

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RESULT
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STRAIN-C-125 / JCM 9153;
TAKAMI H., NAKASONE K., Takaki Y.;
Takami H., NAKASONE K., Takaki Y.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP001514; BAB05734.1: -
SEQUENCE 193 AA; 21835 MW; DDF2567769F0177D CRC64;
                                                                                                                                                      SEQUENCE FROM N.A.

STRAIN-C-125 / JCM 9153;

STRAIN-C-125 / JCM 9153;

STRAIN-C-125 / JCM 9153;

STRAIN-C-125 / JCM 9153;

SUBMITTED (MAR-2000) to the EMBL/GenBank/DDBJ databases EMBL; AP001508; BAB04081.1; -.

SEQUENCE 187 AA; 21119 MW; CC26403CD0D01456 CRC64;
                                                                                                                                                                                                                                                                                                                                            Bacillus halodurans.
Bacteria; Firmicutes; Bacillus/Staphylococcus
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01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
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Bacteria; Firmicutes; Bacillus/Clostridium
Bacillus/Staphylococcus group; Bacillus.
NCBI_TaxID=86665;
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28.7%;
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Pred.
                                                          Score 182.5; DB Pred. No. 5.7e-07
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No. 4.5e-07
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01-OCT-2000
01-OCT-2000
                                 Actinomycetales;
NCBI_TaxID=1655;
                                                                                Bacteria;
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Bacteria; Firmicutes; Bacacillus/Staphylococcus
NCBI_TaxID=86665;
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BH2127 PROTEIN
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                                                                                                          Actinomyces naeslundii.
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l Similarity 24.1%;
49; Conservation
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                                                                           Firmicutes;
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                                                                                Actinobacteria;
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068213 PRELIMINARY; PRT; 365 AA. 068213; 01-AUG-1998 (TEMBLrel. 07, Created) 01-AUG-1998 (TEMBLrel. 07, Last sequence up 01-NOV-1998 (TEMBLrel. 08, Last annotation putative FIMBLA-ASSOCIATED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-C-125 / JCM 9153;
Takami H., Nakasone K., Takaki Y.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AP001514; BAB05846.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MRTITAVLFISFGLLEMFFPRLQTEYYSFYETRLIDSYEKINRELEAFSNEE---PHLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LMTIAGVVLILVAAYLFAKPHIDNYLHDKDKDEKIEQYDKNVKEQASKDKKQQAKPQ-IP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -RGNRHFSRLPDVTIGDEVFLHTKEETFVYKVTDISIIEPTDVDILDDRDGK-HEITMIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KDKSKVAGYIEIPDADIKEPVYPGPATPEQLNRGVSFAEENESLDDO-NISIAGH---TF 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IDRPNYQFTNLKAAKKGSMVYFKVGNETRKYKMTSIRDVKPTDVGVLDEQKGKDKQLTLI 182
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Pred. No. 0.0037;
6; Mismatches 99;
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Best Local S
Matches 41
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01-JAN-1998
01-JAN-1998
01-JAN-1998
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EMBL; AF019629; AAC13546.1; -.
SEQUENCE 365 AA; 39425 MW; BB17A6A0DA8D5410 CRC
                                                                                                                                                                                                                                                                                                                                                                                            Rishovd A.L.;
Submitted (SEP-1997) to t
EMBL; Y10908; CAA71849.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-ATCC 10987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=ATCC 10987;
Kolstoe A.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus/Staphylococcus
NCBI_TaxID=1396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Bacillus/Clostridium Bacillus/Staphylococcus group; Bacillus.
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STRAIN=T14V;
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                       DDQNISIAGHTFIDRPNYQF----TNL----KAAKKGSMVYFKVGNETRKYKMTSIR--
                                                                                  LKKDKTKAQASPTEIVEERTETEKVFDNNDGTYTKKVYTEP:
                                                                                                                                                                KKWYRYLIQLIVVALIVTSIPLNGLAETAPPFTPSPNSEQSPEVEKKEEKELPDPH-PDQ
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IATED PROTEIN
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-VEAPNAKIVTENTTLEPEFEKTTQDGKYVQFKVKDHTIKYKLMSANGE
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26221 MW;
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. 05, Last sequence upd
. 05, Last annotation u
N PRECURSOR (FRAGMENT).
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Last annotation update)
                                                                                                                                                                                                                                                 Score 106.5; DE Pred. No. 0.56; 33; Mismatches
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Pred. No. 0.03
22; Mismatches
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RESULT P91122

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P91122 P91122; 01-MAY-1997 01-MAY-1997 01-NOV-1998

PRELIMINARY;

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SIMILARITY

HUMAN

(TIEMBLrel. 03, Created)
(TIEMBLrel. 03, Last sequence update)
(TIEMBLRel. 08, Last annotation update)
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01-NOV-1999
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"A set of ordered cosmids and a detailed genetic and the 8 Mb Streptomyces coelicolor A3(2) chromosome.";

MOI. Microbiol. 21:77-96(1996).

EMBL; AL079308; CAB45217.1;

SEQUENCE 352 AA; 37819 MW; D1825C3F2E580711 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=A3(2);
Bentley S.D., Parkhill J.,
Submitted (JUN-1999) to th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murphy L., Harris D.;

"A set of ordered cosmids and a detailed genetic and the 8 Mb Streptomyces coelicolor A3(2) chromosome."; submitted (JUN-1999) to the EMBL/GenBank/DDBJ databas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces cuerror.
Bacteria; Firmicutes; Actinobacteria; Actinobacterio
Bacteria; Firmicutes; Actinobacterio
Bacteria; Firmicutes; Streptomycetaceae;
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                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97000351; PubMed=8843436;
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313 RYITLTTCTPEFTSKYRMIVWGK 335
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                                                                                                                                                              148 GYLMLLFYTYQLWWTNYRAH-----AQANQAASNLQDDWANGKRS-----PGSFEPG
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                                                                                                                                                                                       13 GVVLILVAAYLFAKPHIDNYLHDKDKDEKIEQYDKNVKEQASKDKKQQAKPQIPKDKSKV
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               KQLTLITC-DDYNEKTG-
                                                                                                         QGFALLHIPKLDVVVPIAEGISSKKVLDRGMVGHYAEDGLKTAMPDAKAGNFGLAGHRNT
                                                                                                                                   AGY--IEIPDADIKEPVYPGPATPEQLNRGV--SFAEE--NESLDDQ---NISTAGHTFI 123
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                                                   HGEPFRYIN--KLEPGDPIVVETQDKYFVYKMASILPVTSPSNVSVLDPVPKQSGFKGPG
                                                                              DRPNYQFTNLKAAKKGSMVYFKVGNETRKYKMTSIRDV-KPTDVGVLDEQ-----KGKD
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TEGRAL MEMBRANE PROTEIN.
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                                                                                                                                                                                                                     40;
                                                                                                                                                                                                                    Score 104; DB Pred. No. 1.5; 40; Mismatches
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Actinobacteridae; Streptomyces.
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Q9SS68;
01-MAY-2000
                            PUTATIVE | T12J13.4.
                                                    01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2000 (TrEMBLrel. 14,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnson M., Kershaw J., Kirsten J., Laister N., Latreille P. Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Calla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Waterston R.;
Submitted (NOV-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=BRISTOL N2;
MEDLINE=94150718; PubMed=7906398;
  Arabidopsis thaliana (Mou
Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    watson A., Weinstock L., Wilkinson Sproat J., Wohldman P.,
"2.2 Mb of contiguous nucleotide sequence from chromosome
elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Waterston
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Rhabditidae; Pelode
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                         , Created)
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  Embryophyta;
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  Tracheophyta;
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  Spermatophyta;
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Best Local
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Q9U0N1;
01-MAY-2000
01-MAY-2000
01-MAY-2000
                                                                                                                                                                                                                                                                          Barrell B:
Submitted (SEP-1998) to the ENEL; AL031746: CAB63561.1; -
SEQUENCE 673 AA; 79795 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lin X, Kaul S., Town C.D., Benito M., Creasy T.H., Haar Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barns Bowman C.L., White O., Nierman W.C., Fraser C.M.; "Arabidopsis thaliana chromosome III BAC T12J13 genomic submitted (CCT-1999) to the EMBL/GenBank/DDBJ databases EMBL; AC009327; AAF03465.1; -. ITTERPRO, IPR000008; -.
                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=3D7;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium falciparum Eukaryota; Alveolata; NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transferase
SEQUENCE :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3702;
[1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                 Bowman S.,
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GARP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50004; C2_DOMAIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFAM; PF00168; C2;
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181
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                                                                                                        HDKDKDEKIEQYDKNVKEQASKDKKQQAKPQIPKDKSKVAGYIEIPDADIKEPVYPGPAT
                                                                                HKKDKKEKKEKKDKKEKKD-KKEKKHKKEKKHKKDKKKE-----ENSEVMSLYKTGQHK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KTGVWEKRKI
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PK---NATEHGEENLYEEMVSEINNNAQGGLLLSSP-YQYREQGGCGIISSVH-ETSNDT
                                        PEQLNRGVSFAEEN ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVSVWSEEKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AKNDGSNPVYAKLVIGTNGVKTRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A------TPEQLNRGYSFAEENE--SLD-DQNISIAGHTFIDRPNYQFTNLKAAKK 138
                                                                                                                                                                      1 Similarity
42; Conserv
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                                                                                                                                                                                                                                                                                                                                                               Churcher
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) (TrEMBLrel. 13,
) (TrEMBLrel. 13,
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                                                                                                                                                                    32;
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                                                                                                                                                                    Score 97.5; D
Pred. No. 10;
32; Mismatches
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Last
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Pred. No. 9.1;
24; Mismatches
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RESULT
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Best Local S
Matches 41
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Q06106;
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077788;
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01-NOV-1996 (TrEMBLrel.
01-JUN-2000 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The bovine neurofilament M subunit has a novel set of K normally restricted to NF·H.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO ALL OTHER INTERMEDIATE FILAMENT PROTE EMBL, AF091342; AAC36357.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NF-M.
    Submitted (JUL-1995) to [2]
                                                                                                                         Saccharomycetaceae;
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1998
01-MAY-2000
                                             Nelson
                                                               SEQUENCE FROM N.A.
STRAIN=S288C / AB972;
                                                                                                                                                                   Eukaryota; Fungi; Ascomycota;
                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast)
                                                                                                                                                                                                              P8283.19
                                                                                                                                                                                                                                  HYPOTHETICAL 101.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERPRO; IPRO01664; -. PFAM; PF00038; filament; 1.
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Gearhart D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovidae; Bovinae;
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus (Bovine).
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01-MAY-2000 (TremBLrel.
NEUROFILAMENT-M SUBUNIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KE--PVYPGPATPEQLNRGVSFAEENESLDD---
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                                                                                                                                                                                                                                                                                                                                                                                                                                            EGKEEEQETKEKGS----
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                                                                                                                                                                                                                                KDA PROTEIN P8283.19
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                                                                                                                                               Saccharomyces
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Last annotation updat
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Last annotation update)
                       EMBL/GenBank/DDBJ
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                                                                                                                                                                   Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                      PRT;
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                       databases
                                                                                                                                                                   Saccharomycetales;
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RESULT

QY1H3

ID Y1H3

AC QQ

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DT QQ

OT QQ

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Best Local S
Matches 46
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Best Local
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STRAIN-$288C / AB972;
Jia Y., Cherry J.M.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U32445; AAB68082.1; -.
INTERPRO; IPRO00504; -.
PFAM; PF00076; rrm; 5.
PFONTE; PS00030; RNP_1; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POL.
                                                                                                                                                                                                                                                                                                                                                                    "NON-LTR retrotransposons with unique integration preference downstream of Dictyostelium discoideum transfer RNA genes."; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF134171; AAD43059.1; -... INTERPRO; IPRO0477; -... PFAM; PFO0077; rvt; 1. SEQUENCE 1147 AA; 134731 MW; D497537E1A024517 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=AX4; TRANSPOSON=RET
Szafranski K., Gloeckner G
Rosenthal A., Winckler T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dictyostelium discoideum (Slime mold)
Eukaryota; Dictyosteliida; Dictyostel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1999
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=AX4; TRANSPOSON=RETROTRANSPOSON TRE3-C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9Y1H3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein. SEQUENCE 887 AA; 1
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  333
                                           112
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                                    DQNISIAGHTFIDRPNYQFTNLKAAKKGSMYYFKVGNETRKYKMTSIRDVKPTDVGVLDE
                                                                                                                                                                                                                   TNRLMTIAGVVLILVAAYLFAKPHIDN-YLHD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FAKPHIDNYLHDK------DKDEKIEQYDKNVKEQASKDKKQQAKPQIPKDKSKVAG
  AWDIKLKLHLHQETPSKYLTSILKSRA---
                                                                                 RDYLKKEQNKIKKEKNKRKYVIHKLLGNSDII----
                                                                                                        KD--KKQQAKPQIPKDKSKVAGYIEIPDADIKEPVYPGPATPEQLNRGVS-FAEENESLD 111
                                                                                                                                                                     TNRETTTTTTKLERLPWTLCKEILNNKHIHDGLSELISKNKDKIKSVEEWTK-FKNNVI 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DDANSDEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----DRPNYQFTNLKAAKKGSMVYFKVGNETR-----
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35; Conservative
                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                              Conservative
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134731 MW;
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22.2%;
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. 12, Last sequ
. 13, Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence up
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Pred. No. 23;
86; Mismatches
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Pred.
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23;
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16;
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KDKSIFQIKDKDNKTISD
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                                                                                                                                                                                                                                                                                                    Length 1147;
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377
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Qγ

172 QKGKDKQLTLITCDDYNEKTGVWEKRK 198

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RR RN OCC OCC OCC
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Best Local Similarity 28.1%;
Matches 36; Conservative 1
Bevan
Mewes
                                                                                                  Q9SUA1;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL 85.2 KDA PROTEIN.
T15N24.80 OR AT4G26630.
                                                            Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;

Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                 Q9SUA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            investigating biology.";
Science 282:2012-2018(1998).
EMBL; AL132860; CAB60511.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.
Eukaryota: Metazoa: Nematoda; Chromadorea: Rhabditida; Rhabditidae: Peloderinae: Caenorhabditis.
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01-MAY-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
Y56A3A.32 PROTEIN.
                            SEQUENCE FROM N.A.
                                                 NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFAM; PF00070; pyr_redox; 1.
PRINTS; PR00368; FADPNR.
PRINTS; PR00411; PNDRDTASEI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                142 VYFKVGNE 149
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                                                                                                                                                                                                                                                                                                                                                34 HDKDKDEKIEQYDKNVKEQASKDKKQQAKPQIPKDKSKVAGYIEIPDADIKEPVYPGPA-
   H.W.,
                                                                                                                                                                                                                                                                                      KQAEQPEQAEEKQETKDAEPKEQVDDRQTEEAVHARRAPAAAEEP-----APSTSKADA
                                                                                                                                                                                                                                                                                                            ----TPEQL--NRGVSFAEENESLDDQNISIAGH-----TFIDRPNYQFTNLKAAKKGSM 141
                                                                                                                                                                                                                                                                                                                                     HSKKHEEKHEQKHEE-KEHAEPEKKEEAKPEKP-
              Zimmermann
                                                                                                                                                                                                                                                                                                                                                                                                                                          643 AA;
    Mayer
                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
   K.F.X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                           71257 MW;
               Σ.
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13,
  Grueneisen A.,
, Lemcke K., Sc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                  12;
                                                                                                                                                                                                                                                                                                                                                                                 Score 94; DB
Pred. No. 18;
12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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   Schueller
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on update)
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                                                                                                                                 update)
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   C.;
                                                                                                                                                                                                                                                                                                                                                                                                        Length 643;
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              Bancroft I.,
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Job time: 90 sec
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Best Local
Matches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EU Arabidopsis sequencing project; Submitted (AUG-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAY-1999) [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                NGDENKQVENVEGKEK
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                                                                                        TCDDYNEKTGVWEKRK 198
                                                                                                                  EKETKETDITEADHKKAGKEDIQHEADKANGTKDGNTGDIKEEGTLVDEDKGTDMDEKVE
                                                                                                                                           LKAAKKGSMV---YFKVGNETRKYKMTSIRDVKPTDVG-----VLDEQKGKDKQLTLI 182
                                                                                                                                                                                               IPDADIKEPVYPGPATPEQLNRGVS-----FAEENESLDDQNISIAGHTFIDRPNYQFTN 132
                                                                                                                                                                                                                          AEP -- DNMEIDAQIKKDDEKAETEDKESEVKKNEDNAETQKMEEKVEVTKDEGQAEATNM 104
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24.5%;
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Pred. No. 24;
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Result
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3: 'Cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
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Copyright (c) 1993 - 2000 Compugen Ltd
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  US-09-292-437-3
US-08-827-356-5465
US-09-611-529-6656
US-60-242-578-1023
US-60-257-931-3336
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Sequence 3, Appli
Sequence 5465, Ap
Sequence 6656, Ap
Sequence 1023, Ap
Sequence 3336, Ap
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ALIGNMENTS

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	OY 1 MKKWTURLMTIAGVVLILVAAYLFAKPHIDNYLHDKDKDEKIEQYDKNVKEQASKDKKQQ 60	100.0%; Score 1076; DB 27; Length 20 Similarity 100.0%; Pred. No. 3.1e-96; Si Conservative 0; Mismatches 0; Indels); ORGANISH: Staphylococcus aureus US-09-292-437-3	TYPE: PRT	; SEQ ID NO 3	CURRENT FILING DATE: 1999-04-15	; CURRENT APPLICATION NUMBER: US/09/292,437	FILE REFERENCE: 510015.213	NVENTION: IDENTIFICATION OF SORTASE	••	••	; GENERAL INFORMATION:	; Sequence 3, Application US/09292437	US-09-292-437-3	

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Best Local Similarity
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Sequence 5465, Ap
                                                                                                                                  Matches 204;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,356
FILING DATE: 01-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/014,477
FILING DATE: 01-APR-1996
APPLICATION NUMBER: 60/016,743
FILING DATE: 02-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 207 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Karen J. TITLE OF INVENTION:
                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                           HYPOTHETICAL:
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CITY: Kenilworth
STATE: New Jersey
                                                                                                                                                                                                                              NAME/KEY: misc_feature LOCATION: 1...207
                                                                                                                                                                                                                                                                               ORGANISM:
                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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APPLICATION NUMBER: 60/020,016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
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                                                               {\tt MKKWTNRLMTIAGVVLILVAAYLFAKPHIDNYLHDKDKDEKIEQYDKNVKEQASKDNKQQ}
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George H. Miller
Roberta S. Hare
                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                               Staphylococcus aureus
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99.0%;
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Pred. No. 5.7e-95;
                                                                                                                               Mismatches
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LENGTH: 207
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PRIOR
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CURRENT FILING DATE: 2000-06-30
                                                        NUMBER OF SEQ ID
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ORGANISM: Staphylococcus aureus
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                                                            FILING DATE: 1999-(
APPLICATION NUMBER: FILING DATE: 1999-(
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UMBER: US 09/036,082
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1998-03-06
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1997-04-01
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1998-03-06
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JMBER: US 09/037,934
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                        Sequence 3336, Application GENERAL INFORMATION: APPLICANT: Haselbeck, R
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Best Local Similarity
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Best Local
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APPLICANT: Ohlsen, K. L.
APPLICANT: Zyskind, J. W.
APPLICANT: Zyskind, J. W.
TITLE OF INVENTION: Genes Identified as essential
TITLE OF INVENTION: Staphylococcus aureus
FILE REFERENCE: ELITRA, 017PR2
CURRENT APPLICATION NUMBER: US/60/242,578
CURRENT FILING DATE: 2000-10-23
NUMBER OF SEG ID NOS: 1057
  APPLICANT:
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TYPE: PRT
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Haselbeck,
Ohlsen, KL
Zyskind, JW
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Pred. No. 7.1e-95;
0; Mismatches 2;
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GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PATH99-09A
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US-09-450-969-4904
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SEQ ID NO 3336
LENGTH: 206
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Best Local S
Matches 148
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SEQ ID NO 4904
LENGTH: 203
TYPE: PRT
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Best Local Similarity
Matches 204; Conserv
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APPLICANT: Wall, D
TITLE OF INVENTION: Genes identified as esse
TITLE OF INVENTION: typhimurium, Klebsiella
FILE REFERENCE: ELITRA.017PR4
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nes 148; Conserv
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LITCDDYNEKTGVWEKRKIFVATEV
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                                                                            TFIDRPNYQFTNLKAAKKGSMYYFKVGNETRKYKMTSIRDVKPTDVGVLDEQKGKDKQLT 180
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                                                       TFTDRSHYQFTNLKSAKIGSKVYFKTGNQTRKYKITKIRDVKPTEVKVLDEHPNKKNQLT
                                                                                                                            STPKIPSDKSKMAGYIEVPDAQIKEPVYPGPATPEQLNRGVSFAEGDESLNQQNISIAGH
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72.2%; Pred. No. 6.1e-69;
7ative 25; Mismatches 29;
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99.0%;
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US-09-071-035-486
                                                                                            RESULT
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Sequence 5985, Application US/09134000A
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS
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Best Local Similarity
Matches 52; Conserv
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LENGTH: 251 amino acids
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                                                                                                                                                              168 VLDEQKGKDKQLTLITCDDYNEKTGVWEKRKIFVATEVK 206
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                                                                                                                                            192 LIDDVPGON-MITLITCGDLQATTRIAVQGTLAATTPIK 229
                                                                                                                                                                                                                                                   108 ESLDDQNISIAGHTFIDRPNYQFTNLKAAKKGSMVYFKVGNETRKYKMTSIRDVKPTDVG 167
                                                                                                                                                                                                                  133 QVMGKNNYALASHRTEDGVSL-FSPLERTKKDELIYITDLSTVYTYKITSVEKIEPTRVE 191
                                                                                                                                                                                                                                                                                    74 DFDSVESLSTEAVMKAQFENKNLPVIGAIAIPSVEINLPIFKGLSNVALLT-GAGTMKED 132
                                                                                                                                                                                                                                                                                                                           56
                                                                                                                                                                                                                                                                                                                                                          14 KRGKNWLINSLLVLLFIIGLALIFNNQIRSWVVQQNSRSYAVSKLKPADVKKNMARETTF 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: A. Anders Brookes
REGISTRATION NUMBER: 36
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                                                                                                                                                                                                                                                                                                                       D-----KKQQAKPQIPKDKSKVAGYIEIPDADIKEPVYPGPATPEQLNRGVSFAEEN 107
                                                                                                                                                                                                                                                                                                                                                                                              KKWTNRLMTIAGVVLILVAAYLFAKPHIDNYLHDKDKD----EKIEQYD--KNVKEQASK 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20850
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HP Vectra 486/33
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23.7%;
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Pred. No. 2.5e-07
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; TITLE OF INVENTION: FAECALIS FOR DIAGNOSTICS ANI
; FILE REFERENCE: GTC-005
; CURRENT APPLICATION NUMBER: US/09/134,000A
; CURRENT FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 6810
; SEQ ID NO 5985
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000-5985
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US-09-071-035-298
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Best Local
                                                                                                       TELEFAX: (301)
INFORMATION FOR SEQ
                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
MOLECULE TYPE:
                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
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                                 STRANDEDNESS:
                                                                                                                                      TELEPHONE:
                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                        NAME: A. Anders Brookes
REGISTRATION NUMBER: 36
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                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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CITY: Rockville
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52; Conserv
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                    linear
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23.7%;
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US-60-223-804-29
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SEQ ID NO 29
LENGTH: 284
TYPE: PRT
 Sequence 29, Application US/60223804
GENERAL INFORMATION:
APPLICANT: Adderson, Elisabeth
APPLICANT: Bohnsack, John
TITLE OF INVENTION: GROUP B STREPT
TITLE OF INVENTION: THERAPEUTIC CO
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Best Local
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Adderson, Elisabeth
APPLICANT: Bohnsack, John
TITLE OF INVENTION: GROUP B STREPTOCOCCUS POYPEPTIDES NUCLEIC ACIDS AND
TITLE OF INVENTION: THERAPEUTIC COMPOSITIONS AND VACCINES THEREOF
FILE REFERENCE: 2511-1-001
CURRENT APPLICATION NUMBER: US/09/634,341
CURRENT FILING DATE: 2000-08-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                  147
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                                                                                                                                                                                         179 NGKTLAYQVDQIKTVEPTDTKDLHIESGQD-LVTLLTCTPY 218
                                                                                                                                                                                                                                                                      120
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                                                                                                                                                                                                                                                                                                         90
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                                                                                                                                                                                                                                                                                                                                          61 LQEKMEKKNQELAKKGSNPGLDPFSETQKTTKKPDKSYFESHTIGVLTIPKINVRLPIF- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKKWTNRLMTIAGVVLILVA-----AYLFAKPHIDNYL--------HDKDKDE 40
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                                                                                                                                                                                                                                                                                                                                                                                                                  MKSKKKRRIIDGFMILLLIIGIGAFAYPFVSDALNNYLDQQIIAHYQAKASQENTKEMAE 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MKSKKKRRIIDGFMILLLIIGIGAFAYPFVSDALNNYLDQQIIAHYQAKASQENTKEMAE 60
                                                                                                                                                                                                                                                                    DKTNALLLEKGSSLLEGTSYPTGGTNTHAVISGHRGLPQAKL-FTDLPELKKGDEFYIEV
                                                                                                                                                                                                                                                                                                       GPATPEQLNRGVSFAEENE---SLDDQNISIAGHTFIDRPNYQFTNLKAAKKGSMVYFKV 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPATPEQLNRGVSFAEENE---SLDDQNISIAGHTFIDRPNYQFTNLKAAKKGSMVYFKV 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56;
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GROUP B STREPTOCOCCUS POYPEPTIDES NUCLEIC ACIDS THERAPEUTIC COMPOSITIONS AND VACCINES THEREOF
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25.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.7%; Score 158.5; DB 2 25.3%; Pred. No. 4.6e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 20;
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US-09-292-437-6

US-09-292-437-6

Sequence 6, Application US/09292437

GENERAL INFORMATION:

APPLICANT: Olaf Schneewind

APPLICANT: Sarkis Mazmanian

APPLICANT: Sarkis Mazmanian

APPLICANT: Hung Ton-That

TITLE OF INVENTION: IDENTIFICATION OF SORTASE GEN

FILE REFERENCE: 510015.213

CURRENT APPLICATION NUMBER: US/09/292,437

CURRENT FILLING DATE: 1999-04-15

NUMBER OF SEQ ID NOS: 36

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 6

SEQ ID NO 6

LENGTH: 284

TYPE: PRT
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    밁
                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Enterococcus faecalis US-09-292-437-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 2511-1-001P
CURRENT APPLICATION NUMBER: US/60/223,804
CURRENT FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 29
LENGTH: 284
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local
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TYPE: PRT
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                                         147
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179 NGKTLAYQVDQIKTVEPTDTKDLHIESGQD-LVTLLTCTPY 218
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                                                                                                                       90
                                                                                                                                                               61
                                                                                                                                                                                              41 KIEQYDKNVKEQA------SKDKKQQAKPQIPKDKSKVAGYIEIPDADIKEPVYP 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41
                                                                                                                                                                                                                                                                                  1 MKKWTNRLMTIAGVVLILVA-----AYLFAKPHIDNYL-------HDKDKDE 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKKWTNRLMTIAGVVLILVA-----AYLFAKPHIDNYL-------HDKDKDE 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GNETRKYKMTSIRDVKPTDVGVLDEQKGKDKQLTLITCDDY 187
                                       GNETRKYKMTSIRDVKPTDVGVLDEQKGKDKQLTLITCDDY 187
                                                                             DKTNALLLEKGSSLLEGTSYPTGGTNTHAVISGHRGLPQAKL-FTDLPELKKGDEFYIEV 178
                                                                                                                                                           LQEKMEKKNQELAKKGSNPGLDPFSETQKTTKKPDKSYFESHTIGVLTIPKINVRLPIF- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DKTNALLLEKGSSLLEGTSYPTGGTNTHAVISGHRGLPQAKL-FTDLPELKKGDEFYIEV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KIEQYDKNVKEQA------SKDKKQQAKPQIPKDKSKVAGYIEIPDADIKEPVYP 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MKSKKKRRIIDGFMILLLIIGIGAFAYPFVSDALNNYLDQQIIAHYQAKASQENTKEMAE 60
                                                                                                                     GPATPEQLNRGVSFAEENE---SLDDQNISIAGHTFIDRPNYQFTNLKAAKKGSMVYFKV 146
                                                                                                                                                                                                                                        \tt MKSKKKRRIIDGFMILLLIIGIGAFAYPFVSDALNNYLDQQIIAHYQAKASQENTKEMAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GPATPEQLNRGVSFAEENE---SLDDQNISIAGHTFIDRPNYQFTNLKAAKKGSMVYFKV 146
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                                                                                                                                                                                                                                                                                                                    38; Mismatches
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                                                                                                                                                                                                                                                                                                                                           Score 158.5; DB 2
Pred. No. 4.6e-07;
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Pred. No. 4.6e-07;
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                                                                                                                                                                                                                                                                                                                                                                DB 27;
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                                                                                                                                                                                                                                                                                                                                                            Length 284;
                                                                                                                                                                                                                                                                                                                    37; Gaps
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APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AND SEQUENCES RELATING TO ENTEROCOCCUS
TITLE OF INVENTION: FABCALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-005
CURRENT APPLICATION NUMBER: US/09/134,000A
CURRENT FILING DATE: 1998-08-13
NUMBER OF SEQ ID NO5: 6810
SEQ ID NO 6125
LENGTH: 315
TYPE: PRT
ORGANISM: Enterococcus faecalis
US-09-134-000-6125
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US-09-134-000-6125
Sequence 6125, Application US/09134000A
; GENERAL INFORMATION:
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US-09-107-532-5472
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GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
                  APPLICATION NUMBER: 60/085
FILING DATE: May 14, 1998
PRIOR APPLICATION DATA:
APPLICATION UMBER: 60/0515
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                     SOFTWARE:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          210 NGKTLAYQVDQIKTVEPTDTKDLHIESGQD-LVTLLTCTPY 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 DKTNALLLEKGSSLLEGTSYPTGGTNTHAVISGHRGLPQAKL-FTDLPELKKGDEFYIEV 209
NAME:
                                                                                                                                                                          APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Waltham
STATE: Massacl
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nes 56; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92 LQEKMEKKNQELAKKGSNPGLDPFSETQKTTKKPDKSYFESHTIGVLTIPKINVRLPIF- 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPATPEQLNRGVSFAEENE---SLDDQNISIAGHTFIDRPNYQFTNLKAAKKGSMVYFKV 146
                                                                                                                                                                                                                                                                                                                                                        02354
Ariniello, Pamela Deneke
                                                                                                                                                                                                                                                                                                                                                                                                    Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                           100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                  USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.7%; Score 158.5; DB 15; Length 315; 25.3%; Pred. No. 5.3e-07; tive 38; Mismatches 90; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7308
                                                                                                                                60/ 085598
                                                                60/051571
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APPLICANT: Gwen Liu
APPLICANT: Hung Ton-That ,
APPLICANT: Hung Ton-That ,
APPLICANT: Hung Ton-That ,
TITLE OF INVENTION: IDENTIFICATION OF SORTASE GENE
FILE REFERENCE: 510015.213
CURRENT APPLICATION NUMBER: US/09/292,437
CURRENT FILING DATE: 1999-04-15
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 3.0
DЬ
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                                                                                                                                                                                                                                                   ; LENGTH: 227
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-292-437-4
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US-09-292-437-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09292437 GENERAL INFORMATION:
                                                                                                                                                      Query Match
Best Local Similarity
Matches 47; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (781)893-8277 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: pro
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                  181 VTYLEPNPNEDR-VTLMTCTPKGINTHRFLVYGKRVTFTKSELK 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111 DDQNISIAGHTFIDRPNYQFTNLKAAKKGSMVYFKVGNETRKYKMTSIRDVKPTD---- 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 25.4 hes 57; Conservative
83 PVGGDGTHTVISAHRGLPSAEMFTNLNLVKKGDTFYFRVLNKVLAYKVDQILTVEPDQVT 142
                                                                          32
                                                                                              56 DKKQQAKPQIPKDKSKVAGYIEIPDADIKEPVYPGPATPEQLNRGVSFAEENESLDDQNI 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 TAAETDSSLDVAKIELGDPVGILTIPSISLKLPIYDG-TSDKILENGVGITEGTGDITGG 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKKWTNR--LMTIAGVVLILVAAYLFAKPHIDNYLHDKDKDEKIEQYDKNVKEQASKDKK 58
                                                                        DKNYESLLQI--ENNDIMGYVEVPSIKVTLPIY-HYTTDEVLTKGAG------HLFGSAL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VGVLDEQKGKDKQLTLITCDDYNEKTG---VWEKRKIFVATEVK 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NGKNPLIAGHSGLYKDNL-FDDLPSVKKGEKFYIKVDGEQHAYQIDRIEEVQKDELQRNF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QQAKPQIPKDKSKV----AGYIEIPDADIKEPVYPGPATPEQLNRGVSFAEENESL--- 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGKWIIAFWLLSAVGVLLLMPA--------EASVAKYQQNQQIAAIDRTG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sarkis Mazmanian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Olaf Schneewind
                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
                                                                                                                                                                    14.5%; Score 156; DB 27; 32.6%; Pred. No. 5.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.6%; Score 157.5; DB 25.4%; Pred. No. 5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5472:
                                                                                                                                                      19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; 68
                                                                                                                                                      60;
                                                                                                                                                                                        Length 227;
                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  259;
                                                                                                                                                    18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39;
                                                                                                                                                    Gaps
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